



ORIGIN

us-09-684-383-1.rge

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VERSION AX083554.1 GI:13185364

KEYWORDS

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 2272)

AUTHORS Hoeftel G., Bechold R. and Pohl J.

TITLE Monomeric protein of the IgG-9(b) family.

JOURNAL Patent: WO 011041-A 3 15-FEB-2001;

FEATURES

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Location/Qualifiers

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 Db 2161 TCCATTAATCAATAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 2220  
 Oy 2221 GGTTCCTCTTAAAGCTGAGTAACTTTCTGATGATGATGATGATGATGAT 2272  
 Db 2221 GGTTCCTCTTAAAGCTGAGTAACTTTCTGATGATGATGATGATGATGAT 2272

ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 2272)  
 REFERENCE Monomeric protein of the tgf-beta family  
 TITLE Patent: EP 1074620-A 3 07-FEB-2001;  
 JOURNAL Hygiene AG (CH)  
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 BASE COUNT 510 a 663 c 511 g 585 t 3 others  
 ORIGIN  
 Query Match 99.9%; Score 2269; DB 6; Length 2272;  
 Best Local Similarity 99.9%; Pred. No. 0;  
 Matches 2269; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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 Db 61 TTGAGACCAAGCTCTTGAAGACCTGAGCCCTGAGCTGATTTGCTCAAGAGGCTTC 120  
 Oy 121 CCCAGCAATGACCT 180  
 Db 121 CCCAGCAATGACCT 180  
 Oy 181 CACTCCAGAGCTGCGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 240  
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 Oy 301 CCAGCGGAGCT 360  
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RESULT 7  
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 DEFINITION Sequence 3 from Patent EP1074620.  
 ACCESSION AX137805  
 VERSION AX137805.1 GI:14273976  
 KEYWORDS human.  
 SOURCE







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 Db 33578 GCTT 33575

RESULT 9  
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 VERSION AC022506.32 GI:15809067  
 KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_FULLTOP.  
 SOURCE human.  
 ORGANISM Homo sapiens

## REFERENCE

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.  
 1 (bases 1 to 181272)  
 Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-Osman, F.R., Allen, C.,  
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 Weinstein, G., and Gdbbs, R.

## TITLE

JOURNAL  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

## COMMENT

Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 Project Information  
 Center project name: HADR  
 Center clone name: RP11-181L23  
 Summary Statistics  
 Sequencing program: Phrap; version 0.990329  
 Assembly vector: M13; L08821  
 Consensus quality: 184378 bases at least 40  
 Consensus quality: 188378 bases at least 40  
 Consensus quality: 190626 bases at least 40  
 Estimated insert size: 186079; sum-of-coverage estimation  
 Estimated coverage: 0x in 920 bases; agarose-fp estimation  
 Quality coverage: 7.7x in 920 bases; sum-of-coverage estimation  
 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 7 contigs. The true order of the pieces

- \* is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.
- \* This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1	42978:	contig of 42978 bp in length
42979	43078:	gap of unknown length
43079	78521:	contig of 35443 bp in length
78522	78621:	gap of unknown length
78622	109061:	contig of 30440 bp in length
109062	109161:	gap of unknown length
109162	139561:	contig of 30401 bp in length
139563	138681:	gap of unknown length
139663	157019:	contig of 17357 bp in length
157020	157119:	gap of unknown length
157120	170814:	contig of 13695 bp in length
170815	170914:	gap of unknown length
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SOURCE	1. 181272

	a	c	g	t	others
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Best Local Similarity	99.5%;	Pred. No. 0;		
Matches 1556; Conservative	0;	Mismatches	7;	Indels 1; Caps 1

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Oy	497	CGTGTGACAGGAGGTCCAGCAGGCGAGTCTCATATCTTTGTGAGCTCCCTCCAAAT	556
Db	6369	CGTGTGACAGGAGGTCCAGCAGGCGAGTCTCATATCTTTGTGAGCTCCCTCCAAAT	6428
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Db	6429	ACCACTTGGACCTTGAAGAATGAGAGTCTTTGTCTGGGTCCACATATATACCAACTCACC	6488
Oy	617	TTGGCTACTACAGTACCGTCGGAGGTGGATGGCCAGTGGCGCATCAACTCCGCTAGGG	676
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Oy	737	CAGCTAGCCCAAGACTAGTATCTCTGGGTGGAGCTCCGATAGCCCTTTTGTGGGACGC	796
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Qy	1877	ATCCCTGTTCCCTCTCTGTCTAGTGTCATAGTTCTGTGTGTACTGTGGCTATTTCTGTGTC	1936
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Qy	1937	CCTACACTACCTGAGGCTACCCCTTTCATATGAGCCAGCTCTGCGCTACACTTTCGATTTT	1996
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RESULT 10	
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DEFINITION	Homo sapiens chromosome 12 clone RP11-564P5, WORKING DRAFT
SEQUENCE	SEQUENCE, 29 unordered pieces.

ACCESSION AC018805  
 VERSION AC018805.4 GI:8568931  
 KEYWORDS HTG, HTGS\_PHASE1, HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 185688)  
 AUTHORS Waterston, R.H.  
 TITLE The sequence of Homo sapiens clone  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 185688)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (03-JAN-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 COMMENT On Jun 16, 2000 this sequence version replaced gi:8555245.

Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc/index.shtml>  
 Project Information

Center project name: H\_NH0564P05  
 Summary Statistics

Sequencing vector: M13; 878  
 Sequencing vector: Plasmid; 138  
 Chemistry: Dye-Primer ET; 87% of reads  
 Chemistry: Dye-terminator Big Dye; 13% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 172728 bases at least Q40  
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 Consensus quality: 179092 bases at least Q20  
 Insert size: 21700; agarose-fp  
 Insert size: 18288; sum-of-contigs  
 Quality coverage: 3.63 in Q20 bases; agarose-fp  
 Quality coverage: 4.26 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently  
 consists of 29 contigs. The true order of the pieces  
 is not known and their order in this sequence record is  
 arbitrary. Gaps between the contigs are represented as  
 runs of N, but the exact sizes of the gaps are unknown.  
 This record will be updated with the finished sequence  
 as soon as it is available and the accession number will  
 be preserved.

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## FEATURES

## source

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 REFERENCE 1 (bases 1 to 1624)  
 AUTHORS Fang, J., Wang, S.-O., Smiley, E. and Bonadio, J.  
 TITLE Genes coding for mouse activin beta C and beta E are closely linked and exhibit a liver-specific expression pattern in adult tissues  
 JOURNAL Blochm. Biophys. Res. Commun. 231 (3), 655-661 (1997)  
 MEDLINE 97224404  
 REFERENCE 2 (bases 1 to 1624)  
 AUTHORS Fang, J., Wang, S.-O., Smiley, E. and Bonadio, J.  
 TITLE Direct Submission  
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 AUTHORS Hooten, G., Neidhardt, H., Bechtold, R., and Pohl, J.  
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 JOURNAL BIOPHARM GES ZUR BIOTECHNOLOGI (DE)  
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1161 TAGTAGAGGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 1220
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1164 TGTGTCAGAGGCTGCGGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1223
1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
1221 G 1221
1224 G 1224
1224 G 1224

RESULT 15
AR123395 1558 bp DNA Linear PAT 16-MAY-2001
LOCUS AR123395
DEFINITION Sequence 3 from patent US 6171584.
ACCESSION AR123395
VERSION AR123395.1 GI:14108756
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1. (bases 1 to 1558)
AUTHORS Hotten,G., Neidhardt,H., Bechtold,R., Pohl,J. and Paulista,M.
TITLE Method of treatment with growth/differentiation factors of the
TGF-beta family
JOURNAL Patent: US 6171584-A 3 09-JAN-2001;
FEATURES
Source 1. 1558
Location/Qualifiers
BASE COUNT 340 a 453 c 398 g 367 t
ORIGIN
Query Match 34.4% Score 781; DB 6; Length 1558;
Best Local Similarity 79.9% Pred. No. 6.1e-201;
Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;

```





Copyright 1993 GenCore version 5.1.3  
 using sw mod 18 Million cell updates  
 16...ACTATGATCATGTCCTT 22

On nucleic  
Run on:  
US-09-684-221 residues  
2272 chosen parameters:  
3472872

```

title: perfect score: 1000
Sequence:
Scoring table:
  Match 0%
  Match 100%
  first 45 summaries

```

[illegible]

## SUMMARIES

Form	Description
------	-------------

transforming growth factor- $\beta$  (TGF- $\beta$ ) is a secreted protein that has been implicated in a variety of biological processes, including cell growth, differentiation, and apoptosis. TGF- $\beta$  is a member of the transforming growth factor- $\beta$  (TGF- $\beta$ ) superfamily, which also includes bone morphogenetic proteins (BMPs), activin, and nodal. TGF- $\beta$  is secreted as a latent complex with latency-associated protein (LAP) and is activated by proteolytic cleavage of the latent complex. The active TGF- $\beta$  then binds to a heterotetrameric complex of type I and type II receptors, which activates a signaling pathway involving Smad proteins. TGF- $\beta$  has been implicated in a variety of biological processes, including cell growth, differentiation, and apoptosis. TGF- $\beta$  is a member of the transforming growth factor- $\beta$  (TGF- $\beta$ ) superfamily, which also includes bone morphogenetic proteins (BMPs), activin, and nodal. TGF- $\beta$  is secreted as a latent complex with latency-associated protein (LAP) and is activated by proteolytic cleavage of the latent complex. The active TGF- $\beta$  then binds to a heterotetrameric complex of type I and type II receptors, which activates a signaling pathway involving Smad proteins.

ALIGNMENTS

194.2	8.5	26.99	23	AN517574
194.2	7.6	8.25	20	AN378238
172.4	6.8	9.25	19	AN310891
153.8	6.7	12.87	12	AN364607
153	6.3	16.16	12	AN316883
142.4	6.2	24.19	17	AN382440
140.2	6.2	1.66	19	AN103316
138.6	6.1	1.96	8	AN170318
125.6	5.5	1.53	8	AN170317
118.8	5.2	3.58	8	AN160427
118	5.1	9.58	7	AN165753
116.2	4.8	16.20	22	AN505008
108.4	4.8	14.16	22	AN105442
108.4	4.8	14.25	7	AN160429
108.4	4.8	18.73	11	AN170315
108.2	4.7	16.30	22	AN160845
107.2	4.7	3.91	22	AN158656
101.2	4.6	15.05	12	AN108230
101	4.4	16.67	12	AN178839
85.4	3.7	5.09	9	AN206688
72.6	3.5	13.87	13	AN245675
72.6	3.2	13.87	21	AN206689
71.6	3.2	27.11	13	AN096207
71.6	3.2	9.26	16	AN093085
71.6	3.2	9.26	16	AN183316
71.6	3.2	9.26	16	AN096315
71.6	3.2	13.45	12	AN190390
71.6	3.2	13.45	18	AN183317
71.6	3.2	13.45	22	AN190339
69.8	3.1	35.85	16	AN183320
69.8	3.1	35.85	22	AN593562
69.2	3.0	12.33	16	AN096226

Mouse CLASP-1 nuci  
DNA encoding novel  
DNA encoding nress  
human gene exlrv  
human liver activ  
Encodes Xenopus Bo  
Murine full-length  
Human growth diffc  
Human liver activ  
Human liver activ  
Sequence encoding  
Sequence encoding  
Sequence encoding  
Sequence encoding  
Human pntcrass cel  
Angiotensin conver  
Human reproducing  
Human encoding hum  
Sequence encoding  
BDF-3 gene for  
Sequence encoding  
Sequence growth diffc  
Human polynucleo Bo  
Human Xenopus  
Encodes Xenopus  
Nucleotide sequenc  
GDF-1a cDNA sequen  
GDF-1a G11a1 cell 1  
Murine GDF-1 and 1  
Murine gene morphog  
Human bone morphog  
Human bone morphog  
Human bone morphog  
Human bone morphog  
Human bone morphog  
Human bone morphog  
Plasmd PALV1-781  
Plasmd PALV1-781  
DNA encoding novel  
Fusion Of BMP-2 p

RESULT 1	
ID	AAT11104 standard; cDNAs: 2272 bp.
XX	AAT11104
XX	AAT11104:
XX	AAT11104:
DT	09-AUG-1996 (first entry)
XX	Induction; promotion
XX	dental implantation
DE	Transforming growth factor beta MP-121 cDNA.
XX	TGF-beta: MP-121; mitogen; differentiation;
KM	maintenance; morphogen; tissue regeneration;
KM	wound healing; ss.
XX	Homo sapiens.
OS	location/Qualifiers
XX	138..1186
FH	/tag= a TGF-beta-MP-121
FT	/product=
FT	836..1183
FT	/tag= b
FT	mat_peptide
FT	
XX	DEL9511243-Al.
EN	
XX	04-JAN-1996.
PD	95DE-1011243.
XX	27-MAR-1995:
PF	94DE-1423190.
XX	01-JUL-1994:
PK	94DE-1423190.
XX	(BIOP-) BIOPHRM GES BIOTECHNOLOGISCHEN ENTWICKLT.
PA	

Result	No.	Score	Match	Length	DB	ID
			99.9	2272	17	AA711104
	1	2270.4	99.9	2272	16	AA714441
	2	2269	99.9	1837	19	AAV58257
	3	893.8	36.7	10708	12	AAK52730
	4	583.4	25.9	1606	14	AAO47712
	5	271	11.7	265	22	AAAS5132
C	5	265	11.6	1783	22	AA160412
C	7	263.4	11.6	3676	16	AAV19615
C	8	263.4		254		
C	9	254	11.2			

[illegible]

Novel monomeric protein of transforming growth factor-beta family for  
or therapy of diseases associated with bone, cartilage of  
wound healing, has substitution or deletion of

PT prevention of war  
PT damage, promotion of  
PT cysteine -  
PT 300, 31pp; English

[illegible][illegible]

slg-peptide  
FT  
FT  
FT

✓ tag- b

sera c polypeptide

Page 4







Qy	437	ACAGGCTTCACCATCAACACAGACTGCTTATTTTCACTTCTCCTGATTAACACT	436
Db	1990	ACAGACTCTTCACGACATCAACACAGCCGGCTCGAGTTCACACTT---CTCTGGTAGAATG	2046
Qy	497	GCTGTGACAGGGAGGCGACAGCCAGCTCGCATGTTCTTTGTGCAGGCTCCCTTCCAAAT	556
Db	2047	GGCAGTGGCGATGAGAGGCTCCGCGACACCCGGCTTCACTGTTCTGTGACAGTTCCCCACAAAT	2106
Qy	557	ACCACCTGACCTTGAAGAATGAGATCCCTTGTCTGGGGTCCACATTAATACCAACTCAC	616
Db	2107	GCCACCCAGACCATGAATATTAAGACTTCTTGCTGAACACATATGACACCAACCTCAC	2166
Qy	617	TTGGCTACTCAGTACCTGCTGAGAGTGAATGCCAGTGGCTGCGCATCAACTCCCCCTAAGG	676
Db	2167	TTTCACAGTCAAGTACAGTGGTGCAGAGTGAATGCCAGTGGCTGGAACAGCTTCTCTGGGA	2226
Qy	677	CTTGAACTCAAGCTGCCTGSCAGCCAGGGGACACTGACCTGAGAGCTGGTACTTTGAAGG	736
Db	2227	CTTGAACTCAAGCTGCTTGGCAGCCAGGGACACCTTACTCTGGAGCTGGTATCCAGAAAGC	2286
Qy	737	CAGGTACCCAGACTCAGTCACTCTGGGTGAGAGCTGCCATATGAGGCTTTTGTGGACGC	796
Db	2287	CAGGTGCCCCACACTTCTTATCTTGGCTGGCTGGTTTCCACAGGCTTTTGTGGACGC	2346
Qy	797	CGGTTGAGAGTTGGGGGGCAACACAGATTCAACCGAGAGGCATCGACTCCAGAGGAGG	856
Db	2347	CAGGTAAAGGTTGAGGGGGAAGCATGGGTTCCGGCGGAGGTATCGATTGCCAGGGGGG	2406
Qy	857	TCCAGCATGTGCTGTGCAGAGAGATTTTTTGTGGACTTCCGTAGATTGGCTGGCAGACG	916
Db	2407	TCCAGCATGTGCTGTGCAGAGAGATTTTTTGTGAGACTTCCGTAGATTGGCTGGCAATGAC	2466
Qy	917	TGATCATCCAGCTGAGGGGTACGCCCATGAACCTTGCTATAGGGCAGTGGCCCATACAC	976
Db	2467	TGATCATCCAGCTGAGGGGTATGGCATGAACCTTGCTATAGGGCAGTGGCCCATACAT	2526
Qy	977	ATTACAGGCATGCTGTGATTTCTGCTGCTCTTTCACACTGCAGTGCCTCAATCTTCTCAG	1036
Db	2527	GTGGCAGGCATGCTGTGAGCTTCTGCTCTCTTTCACACTGCAGTGCCTCAATCTTCTCAG	2586
Qy	1037	GCCAAACAGGTGAGGGCAGCCACTGAGGGGGCTCATGCTGTATACCACGGCCCGGCTC	1096
Db	2587	GCCAAACAGGTGAGGGCAGCCACTGAGGGGGCTCATGCTGTATACCACGGCCCGGCTC	1646
Qy	1097	CCCGTGTCTGCTCTATTAATGACAGGAGACAGCAACTTGTCAAGACTGACATACCTGAC	1156
Db	2647	CCCTGCTTTGCTCTACTATGACAGGAGACAGCAACTTGTCAAGAGCGGATATACCTGAC	2706
Qy	1157	ATGCTAGTAGAGCGCTGTGGGTGACAGTACTGATGTGTATGGGAGGCCCAAGGTTG	1216
Db	2707	ATGCTGTGTGAGCGCTGTGGGTGTAGTACTTATGGGTGTATACAGGCTGCCCTGAGGTAG	2766
Qy	1217	CATGGGAAAACAGCCCTTACAGAGTGCACCTCTTGTAGAGAGGGAATGACCTCATTC	1276
Db	2767	AATGG-----CCTTCCCTCAGAGAGGGGAAACCTCTGTTCC	2801
Qy	1277	TCTGTCCAGATGTGACATCCCTTCTCTAGACATCTTATGGAATTAACCCACCTTGA	1336
Db	2802	ACTTGTCTCCAGATGTGAAACACCTTTCTTAAGCAT-----GCAGACATCCCTCTGTGGA	2855
Qy	1337	CTTGGAAGAACGCTCATCTTAAGCAATCCTGTGCACTTCTTCGACACTACACCTCTT	1396
Db	2856	CTTTCAGGGGATCCACTCTTAAGAGATCACT-----AGTGCACACAGCTTCTTCTC	1909
Qy	1397	TCTTAGGGGATATCCATCCCGGTAGTGCATCCGCGTAAGCCCACTCCAGGGAGCTCAGAC	1456
Db	2910	TCTGTGGACATGTTGACCC---AGTACACCCATCTCTCAGCCTTAAGCTAGAGCTTAAT	2965
Qy	1457	CCATCTCAACCATGAGCAATGCCATCTGTTTCCAGGCAAGACACCTTATAGCTACCT	1516
Db	2966	CGACTGCTCAACCAAGAGATGTCAATTTTGT---CTTGGCAACACACCTTATAGCTTCC	3024
Qy	1517	TTAATAGACCCCAATACCCACTATGCTTCTGTCTCTTCTTACTACTCAATGTGCCCACTGC	1576

Db 3025 TTAGTGAACGATGTAATCTACTGTCCCTCGCACCCTGCCAC -CGGAGCTTCCTATTCC 3083  
OY 1577 AAGATGAGTTTGACACAACCCCCTCCCAATTTTGTGGATCTGCAGAGAGGCCCTTCTT 1636  
Db 3084 AGCATGATGATGCTTCTAGTGTCTCCCTTGAAATTCGTGTGGCTCTCCGAAGAACCCTTCAT 3143  
OY 1637 TGGATTCCACCAGATTAGATCATCTGTCGCCCAA 1671  
Db 3144 CAGGGTCACGACGATCATATTGCTGCTGCCA 3178

RESULT 5  
AAK52736/c  
ID AAK52736 standard; cDNA; 1606 BP.

AAK52736;  
06-NOV-2001 (first entry)  
Human polynucleotide SEQ ID NO 2265.  
Human: cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
OS Homo sapiens.  
XX  
XX  
PN MO200157190-A2.  
XX  
PD 09-AUG-2001.  
XX  
PX 05-FEB-2001; 2001WO-US04098.  
XX  
PR 03-FEB-2000; 2000US-0496914.  
PR 27-APR-2000; 2000US-0560875.  
PR 20-JUN-2000; 2000US-0598075.  
PR 19-JUL-2000; 2000US-0620325.  
PR 01-SEP-2000; 2000US-0654936.  
PR 15-SEP-2000; 2000US-0663561.  
PR 20-OCT-2000; 2000US-0693325.  
PR 30-NOV-2000; 2000US-0728422.  
XX  
PA (HYSEQ-) HYSEQ INC.  
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;  
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Wejherman T, Goodrich R;  
XX WPI: 2001-476283/51.  
DR P-PADB: AAM79603.  
XX  
XX Nucleic acids encoding polypeptides with cytokine-like activities,  
PT useful in diagnosis and gene therapy -  
PT  
XX Claim 1; Page 4608; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activin/inhibin activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.  
Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.



useful in diagnosis and gene therapy -

Claim 1: Page 1259-1260; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK53435) and the encoded polypeptides (AAK78323-AAK80302) that exhibit activity eluting to cytokine, cell proliferation or cell differentiation or which may induce production of other cytokines in other cell populations. The polynucleotides and polypeptides are useful in gene therapy, vaccines or peptide therapy. The polypeptides have various cytokine-like activities, e.g. stem cell growth factor activity, haematopoiesis regulating activity, tissue growth factor activity, immunomodulatory activity and activity/inhibit activity and may be useful in the diagnosis and/or treatment of cancer, leukaemia, nervous system disorders, arthritis and inflammation.

Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666 (AAK80020) are omitted as the relevant pages from the sequence listing were missing at the time of publication.

Sequence 1783 BP; 511 A; 265 C; 519 G; 488 T; 0 other;

Query Match 11.6% Score 263.4; DB 22; Length 1783;  
Best Local Similarity 99.6%; Pred. No. 9.2e-52;  
Matches 264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2008 TTTTGAAGAAGTTAAATTCCTTAATTTTATTCCTGATACCACTACCAATTTACAG 2067  
1602 TATTGAAAGTTAAATTCCTTAATTTTATTCCTGATACCACTACCAATTTACAG 1543  
2068 GGCATATATCTGATGTAATGAAAGAAAGAAAGCAAGCTACACAGATTAAG 2127  
1542 GGCATATATCTGATGTAATGAAAGAAAGAAAGCAAGCTACACAGATTAAG 1483  
2128 ACCTCAGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 2187  
1482 ACCTCAGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1423  
2188 CAACCTGGCTATGACAGCTCTGAAAGAGGTTCTCTTAAAGCTGAGTAACCT 2247  
1422 CAACCTGGCTATGACAGCTCTGAAAGAGGTTCTCTTAAAGCTGAGTAACCT 1363  
2248 TTTGACTATGATCATGCTTCTT 2272  
1362 TTTGACTATGATCATGCTTCTT 1338

RESULT 8  
AA160442/c  
ID AA160442 standard; cDNA: 3678 BP.  
AC AA160442;  
22-OCT-2001 (first entry)  
Human polynucleotide seq ID NO 4431.  
Human; neotropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation; leukaemia; ss.  
Homo sapiens.  
WO200153312-A1.  
26-JUL-2001.  
26-DEC-2000; 2000MO-US34263.  
21-JAN-2000; 2000US-0488725.  
25-APR-2000; 2000US-0552317.

09-JUL-2000; 2000US-0598042.  
19-JUL-2000; 2000US-0620312.  
03-AUG-2000; 2000US-0653450.  
14-SEP-2000; 2000US-0662191.  
19-OCT-2000; 2000US-0693036.  
29-NOV-2000; 2000US-0727344.  
(HYSE-) HYSEQ INC.  
Tang YF, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;  
Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;  
Zhao QA, Zhou P, Goodrich R, Drmanac RT;  
WPI: 2001-442253/47.  
P-PSDB: AAM41286.  
Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -  
Claim 1: SEQ ID NO 4431; 10078pp; English.  
The invention relates to human nucleic acids (AA15798-AA161369) and the encoded polypeptides (AAM38642-AA42213) with neotropic, immunosuppressant and cytostatic activity. The polynucleotides are useful in gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous system, such as peripheral nervous injuries, peripheral neuropathy and localised neuropathies and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager Syndrome. Other uses include the utilisation of the activities such as: immune system suppression, activity/inhibit activity, chemotactic/chemokinetic activity, haemostatic and thrombolytic activity, cancer diagnosis and therapy, drug screening, assays for receptor activity, arthritis and inflammation, leukaemia and C.N.S disorders.  
Note: The sequence data for this patent did not form part of the printed specification.  
Sequence 3678 BP; 1117 A; 550 C; 877 G; 1134 T; 0 other;

Query Match 11.6% Score 263.4; DB 22; Length 3678;  
Best Local Similarity 99.6%; Pred. No. 1.2e-51;  
Matches 264; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

2008 TTTTGAAGAAGTTAAATTCCTTAATTTTATTCCTGATACCACTACCAATTTACAG 2067  
1566 TATTGAAAGTTAAATTCCTTAATTTTATTCCTGATACCACTACCAATTTACAG 1507  
2068 GGCATATATCTGATGTAATGAAAGAAAGAAAGCAAGCTACACAGATTAAG 2127  
1506 GGCATATATCTGATGTAATGAAAGAAAGAAAGCAAGCTACACAGATTAAG 1447  
2128 ACCTCAGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 2187  
1446 ACCTCAGAGATGTAATGTAATGTAATGTAATGTAATGTAATGTAATGTAATG 1387  
2188 CAACCTGGCTATGACAGCTCTGAAAGAGGTTCTCTTAAAGCTGAGTAACCT 2247  
1386 CAACCTGGCTATGACAGCTCTGAAAGAGGTTCTCTTAAAGCTGAGTAACCT 1327  
2248 TTTGACTATGATCATGCTTCTT 2272  
1326 TTTGACTATGATCATGCTTCTT 1302

RESULT 9  
AA119615/c  
ID AA119615 standard; cDNA to mRNA: 254 BP.  
AC AA119615;  
28-JUN-1996 (first entry)

DE Human gene signature HUMGS00682.  
 XX  
 XX Gene signature: messenger RNA; mRNA; relative abundance; frequency;  
 KW human; cloning; mapping; non-biased library; diagnosis; detection;  
 KW cell typing; abnormal cell function; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX MO9514772-A1.  
 PN  
 XX 01-JUN-1995.  
 PD  
 XX 11-NOV-1994. 94MO-JP01916.  
 PF  
 XX 12-NOV-1993. 93JP-0355504.  
 PR  
 XX (MATS/) MATSUBARA K.  
 PA (OKUBO/) OKUBO K.  
 XX  
 PI Matsubara K, Okubo K;  
 XX  
 XX WPI: 1995-206931/27.  
 DR  
 XX  
 XX Identifying gene signatures in 3'-directed human cDNA library - e.g.  
 PT for diagnosis of abnormal cell function, by preparing cDNA that  
 PT reflects relative abundance of corresp. mRNA in specific human  
 PT tissues  
 XX  
 PS Claim 1: Page 432; 2245pp; Japanese.  
 XX  
 XX A single-stranded DNA (or its complementary strand or the corresp.  
 CC double-stranded DNA) which comprises one of the 7837 "GS" sequences  
 CC given in AAT19001-T26837 and which is able to hybridize to part of  
 CC human genomic DNA, cDNA or mRNA is claimed. The GS (Gene signature)  
 CC sequences were obtained from 3'-directed cDNA libraries prepared  
 CC from various human tissues; synthesis of cDNA was initiated from the  
 CC 3'-end of mRNA by using poly(T) as the sole primer. Since the 3'-  
 CC untranslated sequence is unique to a particular mRNA species, almost  
 CC all the 3'-oriented cDNAs hybridize with specific mRNAs. Each library  
 CC is constructed so as to reflect accurately the relative abundance of  
 CC different mRNAs in the particular tissue from which it was derived.  
 CC The appearance frequency of a given GS in a cDNA library can be  
 CC determined (esp. using primers and probes derived from the GS  
 CC sequences) as a means of diagnosing abnormal cell function or for  
 CC recognising different cell types.  
 CC  
 CC Sequence 254 BP; 74 A; 41 C; 46 G; 93 T; 0 other:  
 XX  
 XX  
 XX Query Match 11.2%; Score 254; DB 16; Length 254;  
 XX Best Local Similarity 100.0%; Pred. No. 6.9e-50;  
 XX Matches 254; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 XX  
 OY 2009 TTTGAAAGTTAAATTCCTTAATTTTATTCCTGACCACTACCAATTTACAGG 2068  
 Db 254 TTTGAAAGTTAAATTCCTTAATTTTATTCCTGACCACTACCAATTTACAGG 195  
 OY 2069 GCATATATCTGATGATTAATGAAGAAAAAGAAAGCAAGCTCAACAGATTAAGA 2128  
 Db 194 GCAATATATCTGATGATTAATGAAGAAAAAGAAAGCAAGCTCAACAGATTAAGA 135  
 OY 2129 CCTGAGAAATGATCTTAATTTGACACATTCATTAATCAATAGCTGCACATTTTGC 2188  
 Db 134 CCTGAGAAATGATCTTAATTTGACACATTCATTAATCAATAGCTGCACATTTTGC 75  
 OY 2189 AAAGTGGCTATGACAGCTCGAACAAGAAAGAGCTTTCTGTTTAAAGCTGACATCTT 2248  
 Db 74 AAAGTGGCTATGACAGCTCGAACAAGAAAGAGCTTTCTGTTTAAAGCTGACATCTT 15  
 OY 2249 TCTGACTATGATC 2262  
 Db 14 TCTGACTATGATC 1

RESULT 10  
 AAC87968/c  
 ID AAC87968 standard; cDNA; 5214 BP.  
 XX  
 AC AAC87968;  
 XX  
 XX 07-MAR-2001 (first entry)  
 DT  
 XX  
 XX Mouse CLASP-1 nucleotide sequence SEQ ID NO:2.  
 DE  
 XX  
 XX CLASP-1; CLASP-2; transmembrane protein; immune response; inflammatory;  
 KW cadherin-like asymmetry protein; autoimmune disease; immunosuppressive;  
 KW immunomodulatory; antiinflammatory; antirheumatic; cyostatic;  
 KW hypotensive; antirheumatic; antinaemic; haemostatic; neutroprotective;  
 KW hypersensitivity; transplantation rejection response; immunodeficiency;  
 KW proliferation; differentiation; inflammatory response; arthritis;  
 KW inflammatory bowel disease; haematopoietic cell; blood protein disorder;  
 KW anaemia; thrombocytopenia; multiple sclerosis; rheumatoid arthritis;  
 KW endometriosis; pregnancy induced hypertension; ss.  
 KW  
 XX  
 OS Mus musculus.  
 XX  
 XX WO200061747-A2.  
 PN  
 XX 19-OCT-2000.  
 PD  
 XX  
 XX 13-APR-2000; 2000MO-US10158.  
 PE  
 XX 14-APR-1999; 99US-0129171.  
 PR 14-MAY-1999; 99US-0134114.  
 PR 14-MAY-1999; 99US-0134117.  
 PR 14-MAY-1999; 99US-0134118.  
 PR 21-OCT-1999; 99US-0160860.  
 PR 29-OCT-1999; 99US-0162498.  
 PR 13-DEC-1999; 99US-0170453.  
 PR 14-JAN-2000; 2000US-0176195.  
 PR 14-FEB-2000; 2000US-0182296.  
 PR  
 XX  
 PA (ARBO-) ARBOR VITA CORP.  
 XX  
 XX Lu PS:  
 XX  
 XX WPI: 2000-619230/59.  
 DR P-PSDB; AAB36521.  
 DR  
 XX  
 XX Isolated cadherin-like asymmetry protein-2 polynucleotide and  
 PT polypeptide used to diagnose, treat and prevent autoimmune diseases and  
 PT inflammatory responses -  
 XX  
 PS Claim 1: Page 271-276; 286pp; English.  
 XX  
 XX The present invention describes cadherin-like asymmetry protein-2  
 CC (CLASP-2). CLASP-2 can have immunosuppressive, immunomodulatory,  
 CC antiinflammatory, antirheumatic, cyostatic, hypotensive, antirheumatic,  
 CC antinaemic, haemostatic and neutroprotective activities. CLASP-2 can be  
 CC used to inhibit an immune response in a subject by interfering with the  
 CC ability of a CLASP-2 protein to bind to another T cell or B cell. An  
 CC immune response in a subject may also be inhibited by administering an  
 CC antibody which specifically binds to CLASP-2. CLASP-2 polynucleotides,  
 CC proteins and antibodies can be used to prevent or treat a CLASP-2  
 CC mediated disease, such as an autoimmune disease caused or exacerbated  
 CC by increased activity of TH1 cells. They can also be used to treat  
 CC hypersensitivities, prevent transplantation rejection responses and  
 CC augment immune responsiveness in immunodeficiency states, inhibit  
 CC proliferation and differentiation of cells involved in an inflammatory  
 CC response e.g., arthritis, inflammatory bowel disease and increase  
 CC differentiation and proliferation of haematopoietic cells e.g., to treat  
 CC anaemia, thrombocytopenia and other blood protein disorders. Disorders  
 CC treated by disrupting CLASP-2 function include multiple sclerosis,  
 CC rheumatoid arthritis, endometriosis and pregnancy induced hypertension.  
 CC The present sequence encodes mouse CLASP-1 which is used in the  
 CC exemplification of the present invention.





polypeptide (II) sequences. (I) is useful as hybridization probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations in responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention.

Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPRO at ftp.wipro.int/pub/published\_poc\_sequences.

Sequence 899 BP; 239 A; 116 C; 285 G; 259 T; 0 other;

Query Match 7.6%; Score 172.4; DB 23; Length 899;  
Best Local Similarity 93.9%; Pred. No. 1.4e-30;  
Matches 201; Conservative 0; Mismatches 11; Indels 2; Gaps 2;

OY 2008 TTGGAAGAGTTAAATTCCTTAATTTTATCTGCTGACCTACCAATTTACAGG 2068  
DB 899 TTGGAAGAGTTAAATTCCTTAATTTTATCTGCTGACCTACCAATTTACAGG 840  
OY 2068 GCAATATCCCTGATTAAGAAAAGAAAAGAAAAGCAAGCTACAGATTAAGA 2128  
DB 839 GCAATATCCCTGATTAAGAAAAGAAAAGAAAAGCAAGCTACAGATTAAGA 780  
OY 2129 CCTCAGGATCTACATCTAATGACCTACATTCG-ATTATCAATAGCTGCCTTTTG 2187  
DB 779 CCTCAGGATCTACATCTAATGACCTACATTCG-ATTATCAATAGCTGCCTTTTG 720  
OY 2188 C-MAACTGTGGCTATGACAGCTCCTGAACAAG 2220  
DB 719 CMAACTGTGGCTATGACAGCTCCTGAACAAG 686

RESULT 13  
AA217574/C  
ID AA217574 standard; cDNA: 825 BP.

XX AA217574:  
DT 12-OCT-1999 (first entry)

DE Human gene expression product cDNA sequence SEQ ID NO:5047.

XX Human: gene: gene expression product; diagnosis: therapy: probe;  
KM detection: mapping: tissue typing: profiling; forensics: cancer;  
XX genetic analysis: colorectal cancer; breast cancer; lung cancer; ss.

OS Homo sapiens.

PN MO9938972-A2.

XX 05-AUG-1999.

PF 28-JAN-1999; 99WO-US01619.

PR 03-APR-1998; 98US-0080666.

PR 28-JAN-1998; 98US-0022910.

PR 24-FEB-1998; 98US-0075954.

PR 31-MAR-1998; 98US-0080114.

PR 03-APR-1998; 98US-0080515.

XX (CHIR) CHIRON CORP.

PA (HYSE-) HYSRO INC.

XX Crkvenjakov R, Dickson M, Drmanac R, Drmanac S;  
PI Escobedo J, Garcia PD, Garcia V, Giese K, Imis MA;  
PI Jones WD, Kassam A, Kennedy GC, Kita D, Labat I;  
PI Lamson G, Leshkowitz D, Pot D, Randazzo F, Reinhard C;  
PI Stache-Grain B, Suduth-Klinger J, Williams LT;  
DR WPI: 1999-494092/41.

PT Novel human genes and their expression products which are  
PT differentially expressed in different cell types

PS Claim 1: Page 2400-2401; 2479pp: English.

CC The present invention describes a library of human polynucleotides  
CC comprising the sequences given in AA212532 to AA217779. Also described is  
CC a method of detecting differentially expressed genes correlated with the  
CC cancerous state of a mammalian cell, comprising detecting at least one  
CC differentially expressed gene product in a test sample from a cell  
CC suspected of being cancerous, where the gene product is encoded by one  
CC of the 5248 polynucleotide sequences given in AA212532 to AA217779. The  
CC polynucleotides can be used as a source of primers and probes, which can  
CC be used for a variety of purpose, e.g. detection of expression levels,  
CC detection of polymorphisms. Polypeptides encoded by the polynucleotides  
CC can be used for raising antibodies for experimental, diagnostic and  
CC therapeutic purposes. The polynucleotides may also be used to construct  
CC arrays for diagnostics (which may be used to determine function of an  
CC encoded protein); and to detect differences in expression levels between  
CC two cells (e.g. to identify abnormal or diseased tissue in a human, to  
CC identify a genetic predisposition or susceptibility to a disease such as  
CC cancer). The polynucleotides or the invention are especially used in the  
CC diagnosis, prognosis and management of colorectal cancer, breast cancer,  
CC and lung cancer. The polynucleotides can also be used to screen for  
CC peptide analogues and antagonists.

Sequence 825 BP; 239 A; 120 C; 162 G; 252 T; 52 other;

Query Match 6.8%; Score 153.8; DB 20; Length 825;  
Best Local Similarity 90.6%; Pred. No. 3.2e-26;  
Matches 231; Conservative 0; Mismatches 14; Indels 10; Gaps 6;

OY 2008 TTGGAAGAGTTAAATTCCTTAATTTTATCTGCTGACCTACCAATTTACAGG 2061  
DB 324 TTGGAAGAGTTAAATTCCTTAATTTTATCTGCTGACCTACCAATTTACAGG 265  
OY 2062 TTACAGGCAATATA-CCTGATCTAATGAAAAGAAAAGAAAAGCAAGCTA-CAACA 2119  
DB 264 TTCCAGGCAATATACCTGATGATTAAGAAAAGAAAAGAAAAGCAAGCTACACCA 205  
OY 2120 GATTAAGAGCT-CAGCAATCTACATCTAATTTGACATTAATTCATTAATGCTG 2178  
DB 204 GATTAAGAGCTCAGCAATCTACATCTAATTTGACATTAATTCATTAATGCTG 145  
OY 2179 CACTTTTGGAAACTGTGGCTATGACAGCTCCTGAACAAGAGG-TTTCCTGTTTAAGCT 2237  
DB 144 CACTTTTGGAAACTGTGGCTATGACAGCTCCTGAACAAGAGGTTTCCTGTTTAAGCT 85  
OY 2238 GCAGTAACCTTTTCTG 2252  
DB 84 GCAGTAACCTTTTCTG 70

RESULT 14

AAV38238  
ID AAV38238 standard; cDNA: 2125 BP.

XX AAV38238;

DT 01-FEB-1999 (first entry)

DE Murine liver actin beta e polypeptide encoding cDNA.





Gencore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 16:51:16 ; Search time 52.7958 Seconds  
(without alignments)  
10570.520 Million cell updates/sec

Title: US-09-684-383-1  
Perfect score: 2272  
Sequence: 1 CAAGAGCCATGCGCAGCTGC.....ACTATGATCATCTTCTT 2272

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 38353 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database :  
1: Issued\_Patents\_NA.\*  
2: /cgn2\_6/ptodata/1/ina/5A\_COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/6B\_COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/Backfiles1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2272	100.0	2272	1	US-08-482-577B-1
2	2272	100.0	2272	3	US-08-289-222E-2
3	2272	100.0	2272	4	US-09-218-176-1
4	2272	100.0	2272	4	US-09-054-526B-2
5	781	34.4	1558	1	US-08-482-577B-3
6	781	34.4	1558	4	US-08-218-176-3
7	265	11.7	265	3	US-09-218-176-3
8	265	11.7	265	4	US-09-054-526B-5
9	142.4	6.3	687	1	US-08-455-550-2
10	140.2	6.2	360	2	US-08-274-215A-11
11	140.2	6.2	360	2	US-08-765-662-11
12	140.2	6.2	360	3	US-09-184-933-11
13	140.2	6.2	360	5	PCT-US95-08745-11
14	140.2	6.2	2419	5	PCT-US95-08745-13
15	140.2	6.2	2419	5	PCT-US95-08745-13
16	125.6	5.5	1966	1	US-08-197-792-44
17	125.6	5.5	1966	1	US-08-459-850-44
18	125.6	5.5	1564	1	US-08-459-214-44
19	119.2	5.2	1524	1	US-08-197-792-34
20	119.2	5.2	1524	1	US-08-459-850-34
21	119.2	5.2	1524	1	US-08-459-214-34
22	118	5.2	3588	1	US-08-197-792-32
23	118	5.2	3588	1	US-08-459-850-32
24	108.4	4.8	1633	1	US-08-459-214-32
25	108.4	4.8	1633	1	US-08-197-792-42
26	108.4	4.8	1633	1	US-08-459-850-42
27	108.4	4.8	1633	1	US-08-459-214-42

28	92.8	4.1	7218	1	US-08-232-463-14	Sequence 14, Appl
29	83.4	3.7	1667	1	US-08-455-550-1	Sequence 1, Appl
30	71.6	3.2	926	3	US-08-362-670B-1	Sequence 1, Appl
31	71.6	3.2	926	3	US-08-333-576C-1	Sequence 1, Appl
32	71.6	3.2	926	4	US-08-808-324-1	Sequence 1, Appl
33	71.6	3.2	926	5	PCT-US94-14030A-1	Sequence 1, Appl
34	71.6	3.2	1345	1	US-08-362-670B-33	Sequence 33, Appl
35	71.6	3.2	1345	4	US-08-808-324-33	Sequence 33, Appl
36	71.6	3.2	1345	5	PCT-US94-14030A-33	Sequence 33, Appl
37	71.6	3.2	1345	5	US-08-362-670B-9	Sequence 9, Appl
38	69.8	3.1	3585	3	US-08-333-576C-9	Sequence 9, Appl
39	69.8	3.1	3585	4	US-08-808-324-9	Sequence 9, Appl
40	69.8	3.1	3585	5	PCT-US94-14030A-9	Sequence 9, Appl
41	69.8	3.1	3585	5	US-08-362-670B-27	Sequence 27, Appl
42	69.2	3.0	1233	1	US-08-333-576C-27	Sequence 27, Appl
43	69.2	3.0	1233	4	US-08-808-324-27	Sequence 27, Appl
44	69.2	3.0	1233	5	PCT-US94-14030A-27	Sequence 27, Appl
45	69.2	3.0	1233	5	PCT-US94-14030A-27	Sequence 27, Appl

## ALIGNMENTS

RESULT 1  
US-08-482-577B-1  
Sequence 1, Application US/08482577B

Patent No. 5807713

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE

APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESS: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM

STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,

STREET: SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/482,577B

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: KLESNER, SHARON

REGISTRATION NUMBER: 36,335

REFERENCE/DOCKET NUMBER: P564-5010

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 2272 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-482-577B-1

Query Match 100.0%; Score 2272; DB 1; Length 2272;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 CAAGAGCCATGCGCAGCTGCAGCAGCACTTCTTCCAGGCGCTTGGCAGCCAGCAGAG 60

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Db 1 CAAGAGCATTGGAGCTGGACACACACTTCTCCAGGGCTCTGGAGCCGAGCAGACAG 60  
OY 61 TTGAGACACAGCTTTGAGACCTGAGCCCTGAGTGTATGTTGCTCAAGAGGCGCTTC 120  
Db 61 TTGAGACACAGCTTTGAGACCTGAGCCCTGAGTGTATGTTGCTCAAGAGGCGCTTC 120  
OY 121 CCCAGCAATGACCTCCCTGATTTGCTTGGCTTTCTCTCTGGCTCCAAACAGAGTGGC 180  
Db 121 CCCAGCAATGACCTCCCTGATTTGCTTGGCTTTCTCTCTGGCTCCAAACAGAGTGGC 180  
OY 181 CACTCCAGAGCTGGGGGTGCTAGTCCAGCATGTGGGGGGCCCACTTGGAGACTGGAGAG 240  
Db 181 CACTCCAGAGCTGGGGGTGCTAGTCCAGCATGTGGGGGGCCCACTTGGAGACTGGAGAG 240  
OY 241 CCAGCGGGAGCTCTTCTTGTATGTGGCCAAAGAGCATCTTGACAACTGACACTTCAC 300  
Db 241 CCAGCGGGAGCTCTTCTTGTATGTGGCCAAAGAGCATCTTGACAACTGACACTTCAC 300  
OY 301 CCAGCGCCCAACACTGACCCGCTGTGTCAGAGCTGCTTTTGAAGACTGACAGCA 360  
Db 301 CCAGCGCCCAACACTGACCCGCTGTGTCAGAGCTGCTTTTGAAGACTGACAGCA 360  
OY 361 CCTCCAGGGGTCCACAGAGGGGCACTTCTAGAGACACAGGAAACAGGAATGTGAAT 420  
Db 361 CCTCCAGGGGTCCACAGAGGGGCACTTCTAGAGACACAGGAAACAGGAATGTGAAT 420  
OY 421 CATCAGCTTGTGAGACAGGCGCTCTCCACACATCAACAGACTCGTCTTATTTTCACTT 480  
Db 421 CATCAGCTTGTGAGACAGGCGCTCTCCACACATCAACAGACTCGTCTTATTTTCACTT 480  
OY 481 CTCTCTGATAGAACTGCTGTGTGACAGGAGGTCCAGCGCCAGCTGCTGTGGTCCACA 540  
Db 481 CTCTCTGATAGAACTGCTGTGTGACAGGAGGTCCAGCGCCAGCTGCTGTGGTCCACA 540  
OY 541 GCAGCTCCCTTCCAAATACCACTTGAAGTGAAGTGCCTTGTGGTGGTCCACA 600  
Db 541 GCAGCTCCCTTCCAAATACCACTTGAAGTGAAGTGCCTTGTGGTGGTCCACA 600  
OY 601 TAATACCAACCTGACCTTGGCTGACTGATGCTGAGAGTGTGATGCCAGTGGTGGCA 660  
Db 601 TAATACCAACCTGACCTTGGCTGACTGATGCTGAGAGTGTGATGCCAGTGGTGGCA 660  
OY 661 TCAACTCCCTAGGGCTGAAAGTCAAGTGTGCTGAGCGCCAGGGGCACTGACCTGGA 720  
Db 661 TCAACTCCCTAGGGCTGAAAGTCAAGTGTGCTGAGCGCCAGGGGCACTGACCTGGA 720  
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Db 781 GCTTTTGTGGCAGCCCGGGTGAAGTGGGGGCAACACAGATTCAACGAGAGCAT 840  
OY 841 CGACTGCGCAAGGAGGTGCGAGATGTGCTGCGACAAAGATTTTGTGGACTTCCGTA 900  
Db 841 CGACTGCGCAAGGAGGTGCGAGATGTGCTGCGACAAAGATTTTGTGGACTTCCGTA 900  
OY 901 GATTGGTGGCAGACTGATCAAGCTGAGGGGTACGCACTGAACTCTGCTAGG 960  
Db 901 GATTGGTGGCAGACTGATCAAGCTGAGGGGTACGCACTGAACTCTGCTAGG 960  
OY 961 GCGTGGCCCACTACATACAGGAGTGGCTGATTTGCTGCTTTCACACTGAGT 1020  
Db 961 GCGTGGCCCACTACATACAGGAGTGGCTGATTTGCTGCTTTCACACTGAGT 1020  
OY 1021 GCTCAATCTTCTCAAGGCGCAACAGCTGAGGAGACACACTGGAGGGGCTATGCTGT 1080  
Db 1021 GCTCAATCTTCTCAAGGCGCAACAGCTGAGGAGACACACTGGAGGGGCTATGCTGT 1080  
OY 1081 ACCCAGCGCGCGCGCGCTCTCTGCTCTATATGAGAGGAGCAACATTTGCA 1140  
Db 1081 ACCCAGCGCGCGCGCGCGCTCTCTGCTCTATATGAGAGGAGCAACATTTGCA 1140  
|||||  
Db 1081 ACCCAGCGCGCGCGCGCGCGCTCTCTGCTCTATATGAGAGGAGCAACATTTGCA 1140  
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Db 1141 GACTGACATACCTGACATGATAGAGGCTGTGGTGGAGTACTATGTGTAT 1200  
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Db 1201 GGGCAGCCCAAGGTGATGGGAAACAGCCCTTACAGAAAGTCACTTCTTGAAGGA 1260  
OY 1261 GGGAAATGACCTATTTCTGTCCAGAAATGAGACTCCCTTCTGAGCATTTATGGA 1320  
Db 1261 GGGAAATGACCTATTTCTGTCCAGAAATGAGACTCCCTTCTGAGCATTTATGGA 1320  
OY 1321 ATTACCCCACTTTGACTTGAAGAAACCTTCACTAAAGCAAGTCACTGCGCATTC 1380  
Db 1321 ATTACCCCACTTTGACTTGAAGAAACCTTCACTAAAGCAAGTCACTGCGCATTC 1380  
OY 1381 TGACCACTACCTCTTCTAGGGGATAGTCCATCCCGGTAGTCCATCCGCTAGCCCA 1440  
Db 1381 TGACCACTACCTCTTCTAGGGGATAGTCCATCCCGGTAGTCCATCCGCTAGCCCA 1440  
OY 1441 CTCAGGAGCTCAGACCCATCTCCAAACATGAGCAATGCGCATGTGCTCCAGCAAGA 1500  
Db 1441 CTCAGGAGCTCAGACCCATCTCCAAACATGAGCAATGCGCATGTGCTCCAGCAAGA 1500  
OY 1501 CACCTTACCTACCTTTATAGACCCCATTAACCCACATATGCTTCTCTTCTACT 1560  
Db 1501 CACCTTACCTACCTTTATAGACCCCATTAACCCACATATGCTTCTCTTCTACT 1560  
OY 1561 CAATGTGCCCACTTCAAGATAGTGTGACACAAACCCCTTCCCAATTTTGTGGATTC 1620  
Db 1561 CAATGTGCCCACTTCAAGATAGTGTGACACAAACCCCTTCCCAATTTTGTGGATTC 1620  
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OY 1681 TACCTACCCCTCTCTGCTGTGAGACCCCTGCTCTTCTTCTTCTGAGAGTACTA 1740  
Db 1681 TACCTACCCCTCTCTGCTGTGAGACCCCTGCTCTTCTTCTTCTGAGAGTACTA 1740  
OY 1741 AAGCTCTCTTGTGATACCTTATCATCTTTTGTGCTCTGCTCTCTCTCTCTCT 1800  
Db 1741 AAGCTCTCTTGTGATACCTTATCATCTTTTGTGCTCTGCTCTCTCTCTCTCT 1800  
OY 1801 AAGGGTGAATGCTGAGCTCTATCACTGAGTCCCTGCTGCTGCTGCTGCTGCT 1860  
Db 1801 AAGGGTGAATGCTGAGCTCTATCACTGAGTCCCTGCTGCTGCTGCTGCTGCT 1860  
OY 1861 GGTGAGGCGATTTCTTATCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
Db 1861 GGTGAGGCGATTTCTTATCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
OY 1921 GTGGCTATTTCTGTGCTCTACACTGAGTGGCTACCCCTTCCAGAGGCGCTGCT 1980  
Db 1921 GTGGCTATTTCTGTGCTCTACACTGAGTGGCTACCCCTTCCAGAGGCGCTGCT 1980  
OY 1981 ACATTTGATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2040  
Db 1981 ACATTTGATTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTT 2040  
OY 2041 TCTGTGACACATACAGCAATTTACAGGGCAATATACCTGATTAAGAAAGAAAGA 2100  
Db 2041 TCTGTGACACATACAGCAATTTACAGGGCAATATACCTGATTAAGAAAGAAAGA 2100  
OY 2101 AAAAGCAAGCTACAAAGATTAAGAGCTGAGAAATGATCACTTAATGACACTACAT 2160  
Db 2101 AAAAGCAAGCTACAAAGATTAAGAGCTGAGAAATGATCACTTAATGACACTACAT 2160  
OY 2161 TGCATTAATCAATAGCTGACTTTTGAAGCTGTGCTATGAGCTGCGCAAGAG 2220  
Db 2161 TGCATTAATCAATAGCTGACTTTTGAAGCTGTGCTATGAGCTGCGCAAGAG 2220





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 DB 1201 GGGAGCCCAAGTTGGATGGGAAACACGCCCTACAGAAAGTGCATCTCTTGAGAGGA 1260  
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 DB 1261 GGGAAATGACCTATCTCTGTCAGAAATGTGGAGTCCCTCTTCCGAGACATCTTATGAA 1320  
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 DB 1321 ATTACCCGACCTTGTGACTTGAGAAACCTTCATCTAAAGCAAGTCACTGTGCATCTTCC 1380  
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 DB 1381 TGACCACTACCTCTTCTTCCAGGCAATAGTCATCCGCTAGTCCATCCGCTAGCCCA 1440  
 QY 1441 CTCACAGGAGTACAGACCATCTCCAAACATGAGCAATGCAATGCAATGCAATGCAATGCA 1500  
 DB 1441 CTCACAGGAGTACAGACCATCTCCAAACATGAGCAATGCAATGCAATGCAATGCAATGCA 1500  
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 DB 1621 CAGAGAGGCCCTTCTTGTGATTCACCAAGTTAGATCACTGCTGCCCAATTTAGAGCT 1680  
 QY 1681 TACCTACCCCTCTTCTTGTGAGGCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
 DB 1681 TACCTACCCCTCTTCTTGTGAGGCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1740  
 QY 1741 AAGCTCTCTTGTGATTCACCTATCCCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800  
 DB 1741 AAGCTCTCTTGTGATTCACCTATCCCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1800  
 QY 1801 AAGGCTGACTTGTGATTCACCTATCCCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860  
 DB 1801 AAGGCTGACTTGTGATTCACCTATCCCTATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1860  
 QY 1861 GGTGAGGCAATTTCTTATCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
 DB 1861 GGTGAGGCAATTTCTTATCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1920  
 QY 1921 GTGGCTATTTCTGTCCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 1980  
 DB 1921 GTGGCTATTTCTGTCCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 1980  
 QY 1981 ACATTTGATTT 2040  
 DB 1981 ACATTTGATTT 2040  
 QY 2041 TCCGCTGATTTCTGTCCTTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCTACCT 2100  
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 QY 2101 AAAAGACAAAGCTACACAGATTAAGGACCTCAGGAATGATTAATTTGACCTACAT 2160  
 DB 2101 AAAAGACAAAGCTACACAGATTAAGGACCTCAGGAATGATTAATTTGACCTACAT 2160  
 QY 2161 TGCATTAATCAATAGTGCATTTTGTGCAAACTGTGGCTATGACAGTCTCTGAACAAG 2220  
 DB 2161 TGCATTAATCAATAGTGCATTTTGTGCAAACTGTGGCTATGACAGTCTCTGAACAAG 2220  
 QY 2221 GGTTCCTGTTTAAAGTGCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2272  
 DB 2221 GGTTCCTGTTTAAAGTGCATTTTGTGATGATGATGATGATGATGATGATGATGATGATGAT 2272

RESULT 3  
 US-09-218-176-1  
 ; Sequence 1, Application US/09218176  
 ; Patent No. 6171584  
 ; GENERAL INFORMATION:  
 ; APPLICANT: H TREN, Gertrud  
 ; APPLICANT: NEIDHARDT, Helge  
 ; APPLICANT: BECHTOLD, Rolf  
 ; APPLICANT: POHL, Jens  
 ; APPLICANT: PAULISTA, Michael  
 ; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
 ; NUMBER OF SEQUENCES: 49  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: NIKAI DO, MARCELSTEIN, MURRAY & ORAM LLP  
 ; STREET: 655 Fifteenth Street, N. W., G Street Lobby,  
 ; CITY: Suite 330  
 ; STATE: Washington  
 ; COUNTRY: USA  
 ; ZIP: 20005  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/218.176  
 ; FILING DATE: Herewith  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/679,048  
 ; FILING DATE: 12-JUL-1996  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP96/03065  
 ; FILING DATE: 12-JUL-1996  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/EP93/00350  
 ; FILING DATE: 2-FEB-1993  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/482,577  
 ; FILING DATE: 7-JUN-1995  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: EP 92 102 324.8  
 ; FILING DATE: 12-FEB-1992  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE P 44 23 190.3  
 ; FILING DATE: 01-JUL-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: DE 195 11 243.1  
 ; FILING DATE: 27-MAR-1995  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: KITT, Monica Chlo  
 ; REGISTRATION NUMBER: 36,105  
 ; REFERENCE/DOCKET NUMBER: P564-6010  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202/638-5000  
 ; TELEFAX: 202/638-4810  
 ; INFORMATION FOR SEQ ID NO: 1:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 2272 base pairs  
 ; TYPE: nucleic acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: DNA  
 ; US-09-218-176-1  
 Query Match 100.0%; Score 2272; DB 4; Length 2272;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 2272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 CAAGAGCCATGCGAGTGGACACACACTTCTTCAGGGCCCTGGCAGGACAGAG 60  
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61 TTGAGACACAGCTGTTGAGACCTGAGCCCTGAGTCTGTATTGCTCAAGAGGCTTC 120  
121 CCAGCAATACCTCTCTCATTTGCTTCTGCTTCTCTGCTGCTGCTCAACAGAGTGGC 180  
121 CCAGCAATACCTCTCTCATTTGCTTCTGCTTCTCTGCTGCTGCTCAACAGAGTGGC 180  
181 CACTCCAGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
181 CACTCCAGAGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
241 CCAGCGGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
241 CCAGCGGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
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661 TCAACTCCCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
661 TCAACTCCCTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720  
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1081 ACCCAGCGGCG 1140  
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1441 CTCCAGGAGCTGACACCTATCTCCACCATGAGCAATGCAATGCTGCTGCTGCTGCTGCT 1500  
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1501 CACCTTACCTGACCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
1501 CACCTTACCTGACCTTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1560  
1561 CAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1620  
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1621 CAGAGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1680  
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1861 GGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1920  
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1921 GGTGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1980  
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1981 ACATCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
1981 ACATCTGATTTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2040  
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Db 2161 TGCATTAATCAATAGCTGACCTTTTGCAGAACTGCGCTATGACAGTCTCTGAACAAGAG 2220  
OY 2221 GGTTCGCTTTAGCTGACATTAATTTTCTGACTATGATCATCTTCCTT 2272  
Db 2221 GGTTCGCTTTAGCTGACATTAATTTTCTGACTATGATCATCTTCCTT 2272

## RESULT 4

US-09-054-526B-2  
Sequence 2, Application US/09054526B  
Patent No. 6197550  
GENERAL INFORMATION:  
APPLICANT: H TTEEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
NUMBER OF SEQUENCES: 53  
GROWTH/DIFFERENTIATION FACTORS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI DO, MARMELESTEIN, MURRAY & ORAM LLP  
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054,526B  
FILING DATE: 03-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-8005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
FAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2272 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA from mRNA  
US-09-054-526B-2

Query Match 100.0%; Score 2272; DB 4; Length 2272; %  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 2272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CAAGGACGATGCGAGCTGACACACACTTCTCCAGGCGCTCTGGACGACGAGACGAG 60  
Db 1 CAAGGACGATGCGAGCTGACACACACTTCTCCAGGCGCTCTGGACGACGAGACGAG 60  
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Db 1 TTGAGACACAGCTGTGTAGACCTTGAGCCCTGACTCTGTATGCTCAAGAGGCGCTTC 120

Db 61 TTGAGACACAGCTGTGTAGACCTTGAGCCCTGAGCTGTATGCTCAAGAGGCGCTTC 120  
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Db 121 CCCAGCAATGACCTCCCATATGCTGTGGCTTCTCTCTGCTGCTCCACACAGAGTGC 180  
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OY 301 CCAGCGGAGCTCTCTTCTATCTGCGCAAGAGAGCATCTTGGACAACTGACCTTAC 360  
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DB 1441 CTCACAGGATCTAGACCCATCTCCAAACATGAGCAATGCCATGCTGTCAGCAAGA 1500
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OY 1561 CAATGCTCCCACTCCAAAGATGATGACACACCCCTTCCCAATTTTCTGATCTC 1620
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DB 1621 CAGAGAGCCCTCTTCTTGAATTCACAAAGTTTGAATCAGTCTGCCCCAAATAGAGCT 1680
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DB 1681 TACCTACCCCTCTTCTTGAATTCACAAAGTTTGAATCAGTCTGCCCCAAATAGAGCT 1740
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DB 1801 AAGGCTGATCTGCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTGATCTG 1860
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OY 2101 AAAAGCAAAAGTACACAGATTAAGAGAGCTGAGAGATGATCTGATCTGATCTGATCTG 2160
    |||||
DB 2101 AAAAGCAAAAGTACACAGATTAAGAGAGCTGAGAGATGATCTGATCTGATCTGATCTG 2160
OY 2161 TGCATTAATCAATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
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DB 2161 TGCATTAATCAATAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2220
OY 2221 GGTTCCTGCTTAAAGCTGAGTAACCTTTCTGACTATGATCATCTGCTCTT 2272
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DB 2221 GGTTCCTGCTTAAAGCTGAGTAACCTTTCTGACTATGATCATCTGCTCTT 2272

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RESULT 5
US-08-482-577B-3
Sequence 3, Application US/08482577B
Patent No. 5807713
GENERAL INFORMATION:
APPLICANT: HOTTEN, GERRIUD
APPLICANT: NEIDHARDT, HELGE
APPLICANT: BECHTOLD, ROLE
APPLICANT: POHL, JENS
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESS: NIKAI DO, MARCELSTEIN, MURRAY, AND ORAM
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,
STREET: SUITE 330
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,577B
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KLESNER, SHARON
REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P564-5010
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1558 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: Linear
MOLECULE TYPE: DNA
PUBLICATION INFORMATION:
DOCUMENT NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994
US-08-482-577B-3
Query Match 34.4%; Score 781; DB 1; Length 1558;
Best Local Similarity 79.9%; Pred. No. 5.1e-189;
Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;
OY 24 CACACTCTCTCCAGGCGCTCTGGCAGCCAGACAGATTGAGACACAGCTGTGAGACC 83
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OY 84 CTGAGCCCTGAGTCTGATCTGCTCAAGAAAGGCGCTTCCCGCAATGACCTCTCATYGC 143
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DB 87 CTGATATAGAGCTTTGGGCTCTTAAGAGAGGCTATCTCCAGCAATGAGCTCTCTGTC 146
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Db 241 AGTAGAGGCTGTGGGTGCAGTTAG 265

## RESULT 8

US-09-054-526B-5  
Sequence 5, Application US/09054526B  
Patent No. 6197350  
GENERAL INFORMATION:  
APPLICANT: H. TREN, GERTHARD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
NUMBER OF SEQUENCES: 53  
GROWTH/DIFFERENTIATION FACTORS  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: FLOPPY disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054,526B  
FILING DATE: 03-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTUS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA from mRNA  
US-09-054-526B-5

Query Match 11.7%; Score 265; DB 4; Length 265;  
Best Local Similarity 100.0%; Pred. No. 2,7e-58;  
Matches 265; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 CATCAGCCTGAGGCTAGCGCAGTCTGATAGGAGGAGCCACATACATAGC 60  
QY 982 AGGCATGCCCTGATATGCTCTCTTTCACACTGCACTGCTCAATCTTTCAGAGGCCAA 1041  
Db 61 AGGCATGCCCTGATATGCTCTCTTTCACACTGCACTGCTCAATCTTTCAGAGGCCAA 120  
QY 1042 CACAGCTGACGAGCACCACCTGAGGGGCTCATGCTGTACCCACGCGCCGCT 1101  
Db 121 CACAGCTGACGAGCACCACCTGAGGGGCTCATGCTGTACCCACGCGCCGCT 180  
QY 1102 GTCTCTGCTATTATATACAGGAGCAGCAACATTGTCAAGACTGCATACCTGACATGCT 1161  
Db 181 GTCTCTGCTATTATATACAGGAGCAGCAACATTGTCAAGACTGCATACCTGACATGCT 240  
QY 1162 AGTAGAGGCTGTGGGTGCAGTTAG 1186  
Db 241 AGTAGAGGCTGTGGGTGCAGTTAG 265

## RESULT 9

US-08-455-550-2  
Sequence 2, Application US/08455550  
Patent No. 5670338  
GENERAL INFORMATION:  
APPLICANT: MURAKAMI, KAZUO  
APPLICANT: KATO, YUKIO  
APPLICANT: KATO, YUKIO  
TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DIKE, Bronstein, Roberts & Cushman  
STREET: 130 Water Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/455,550  
FILING DATE: 31-MAY-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/056,564  
FILING DATE: 30-APR-1993  
APPLICATION NUMBER: 07/577,892  
FILING DATE: 05-SEP-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Eisenstein, Ronald I  
REGISTRATION NUMBER: 30628  
REFERENCE/DOCKET NUMBER: 40302-FWC-DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-523-3400  
TELEFAX: 617-523-6440  
TELEX: 200291  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-455-550-2

Query Match 6.3%; Score 142.4; DB 1; Length 687;

Best Local Similarity 60.0%; Pred. No. 5.7e-27;  
Matches 277; Conservative 0; Mismatches 176; Indels 9; Gaps 2;

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OY 772 TGGCCATAGGCTTTTGGGAGAGAGT---TGGGGGCAACACAGATTCA 828
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 67 TTCCCAAGGCTTTGTTGTTAGACAGGCAAGTCCATGACCAATGCTAC 126
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 829 CCGACGAGGATGACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 888
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 127 AAGAGAGGCTTTAGCTGATGATGATGATGATGATGATGATGATGAT 186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 889 GGAATTCCTGATGATGATGATGATGATGATGATGATGATGATGATG 948
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 187 AGACTTCAAGATGATGATGATGATGATGATGATGATGATGATGATG 246
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 949 CTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1008
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 247 TTATTCATGAGGCTTTGCAATGATGATGATGATGATGATGATGAT 306
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1009 TCACACTGAGTGTCTCATCTTCTCAAGGCAACACAGCTGAGGAGG 1068
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 307 CCACACAGGATTTAATTCATTAAGGCCAACA-----ATATCCAGAC 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1069 CTCATGCTGTACCCAGGCGCCGCCCTGTCTGTCTGTCTGTCTGT 1128
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 361 CTCATGCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 420
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1129 CACATGTCAGACTGATGATGATGATGATGATGATGATGATGATGAT 1188
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 421 CACGCTTCTCAAGACTGATGATGATGATGATGATGATGATGATGAT 480
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1189 TATGCTGTGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1230
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 481 CTTGGCTACATGATGATGATGATGATGATGATGATGATGATGATG 522
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 10  
US-08-274-215A-11  
Sequence 11 Application US/08274215A  
Patent No. 5831054

GENERAL INFORMATION:  
APPLICANT: Lee, Se-Jin  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson, P.C.  
STREET: 4225 Executive Square, Suite 1400  
CITY: LA Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/274,215A  
FILING DATE: 13-JUL-1994  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-68-5070  
TELEFAX: 619-68-5099  
INFORMATION FOR SEQ. ID NO: 11:  
SEQUENCE CHARACTERISTICS:

LENGTH: 360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...357

Query Match 6.2%; Score 140.2; DB 2; Length 360;  
Best Local Similarity 65.3%; Pred. No. 1.6e-26;  
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

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OY 844 CTGCCAAGAGGCTCCAGATGCTCTGCAAGAGATTTTGTGGACTCCGAGAT 903
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 24 CTGAGAGCTTGGACCCCTTATGTTGAGCGAGACCATTAAGTACCTTCAGAACT 83
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 904 TGGCTGACGAGCTGATGATGATGATGATGATGATGATGATGATGATG 963
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 84 GGGATGGGAGGAGTGTGATGATGATGATGATGATGATGATGATGATGAT 143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 964 GTGCCACTACATATGACAGGATGCTGTATGCTGCTCTTTCACACTGAGTCT 1023
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 144 GTGCCCTTCCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1024 CAATCTTCTCAAGGCAACACAGCTGACGACCACTGAGGAGGAGGAGGAG 1083
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 204 CAGCTCTCTCAAGCAACATCTT-----TGCCCTCCAGTACTCTCTGTTGCTCC 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1084 CAGCGCCGCGGCCCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCT 1143
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 258 TACTGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
OY 1144 TGACATACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1186
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 318 GATGTGCCAGATATGTTGTTGAGAGCCTGTGCTGAGCTAG 360
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

RESULT 11  
US-08-765-662-11  
Sequence 11 Application US/08765662  
Patent No. 5829213

GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: LA Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,662  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745  
FILING DATE: 12-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099

TELEX:  
: INFORMATION FOR SEQ ID NO: 11:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 360 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: cDNA  
: HYPOTHETICAL: NO  
: ANTI-SENSE: NO  
: FRAGMENT TYPE:  
: ORIGINAL SOURCE:  
: FEATURE:  
: NAME/KEY: Coding Sequence  
: LOCATION: 1..357  
: OTHER INFORMATION:  
: US-08-765-662-11

Query Match 6.2%; Score 140.2; DB 2; Length 360;  
Best Local Similarity 65.3%; Pred. No. 1.6e-26;  
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

OY 844 CTGCCAAGGAGGCTCCAGATGCTGTGTCGACAGAGTTTGTGGACTTCGGTGAAT 903  
DB 24 CTGTGAGCCTGGGACCCCTTATGTTGACAGCGACCATTTACCTAGACTTCCAGAACT 83  
OY 904 TGGCTGGACGATGATGATCCAGCCTGAGGCTACGCAATCTTGCATAGGGCA 963  
DB 84 GGGATGGCGGAGTGTGATGATGACGCGGAGGGTACCACTGATTAAGCACTGGGCA 143  
OY 964 GTGCCACTACACATAGCAGGATGCTGTGATGCTGCTCTTACACTGAGTGT 1023  
DB 144 GTGCCCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203  
OY 1024 CAATCTTCAAGGCGACACAGCCTGAGGAGGAGGCTGATGCTGTGCTGCTGCT 1083  
DB 204 CAGCTCTCTCAAGGCGACAAATCT-----TGGCTGCCAGTACCTCTGTTGTGCTCC 257  
OY 1084 CAGGCGCGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
DB 258 TACTGCGCGAGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317  
OY 1144 TGACATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1186  
DB 318 GGATGTGCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

## RESULT 12

US-09-184-933-11

Sequence 11, Application US/09184933

Patent No. 6130050

GENERAL INFORMATION:

APPLICANT: Lee, Se-Jin

APPLICANT: Esquele, Aurora F.

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson, P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: US

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: Windows95

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/274,215  
FILING DATE: 13-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/040001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-68-5099  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..357  
US-09-184-933-11

Query Match 6.2%; Score 140.2; DB 3; Length 360;  
Best Local Similarity 65.3%; Pred. No. 1.6e-26;  
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

OY 844 CTGCCAAGGAGGCTCCAGATGCTGTGTCGACAGAGTTTGTGGACTTCGGTGAAT 903  
DB 24 CTGTGAGCCTGGGACCCCTTATGTTGACAGCGACCATTTACCTAGACTTCCAGAACT 83  
OY 904 TGGCTGGACGATGATGATCCAGCCTGAGGCTACGCAATCTTGCATAGGGCA 963  
DB 84 GGGATGGCGGAGTGTGATGATGACGCGGAGGGTACCACTGATTAAGCACTGGGCA 143  
OY 964 GTGCCACTACACATAGCAGGATGCTGTGATGCTGCTCTTACACTGAGTGT 1023  
DB 144 GTGCCCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203  
OY 1024 CAATCTTCAAGGCGACACAGCCTGAGGAGGAGGCTGATGCTGTGCTGCTGCTGCT 1083  
DB 204 CAGCTCTCTCAAGGCGACAAATCT-----TGGCTGCCAGTACCTCTGTTGTGCTCC 257  
OY 1084 CAGGCGCGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
DB 258 TACTGCGCGAGGCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317  
OY 1144 TGACATACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1186  
DB 318 GGATGTGCCAGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 360

## RESULT 13

PCT-US95-08745-11

Sequence 11, Application PC/TUS9508745

GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish &amp; Richardson

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

FILING DATE: 12-JUL-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Ph.D., Lisa A  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1..357  
OTHER INFORMATION:  
PCT-US95-08745-11

Query Match  
Best Local Similarity 65.3%; Pred. No. 1,6e-26;  
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

QY 844 CTGCCAAGGAGGCTCCAGATGCTGTCGACAGATTGTTTGGACTCCGTAGAT 903  
DB 24 CTGTGAGGCTCGAGACCCCTTATGTCAGGCGAGACATTAAGTACACTCCAGGAAC 83  
QY 904 TGGCTGGACAGACTGATATCAGCCTGAGGGCTACGCCATGAATTTGCTAGGCA 963  
DB 84 GGGATGGGAGGAGTGGATACAGCCGAGGGGATACAGCAATTAATGCTGAGTGGCA 143  
QY 964 GTGCCACTACATAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023  
DB 144 GTGCCCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 203  
QY 1024 CAATCTTCAAGGCCACACAGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1083  
DB 204 CAGCTCTCTCAAGGCCACACATCT-----TGGCTGCAAGTACCTCTGCTGCTGCT 257  
QY 1084 CAGGCGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
DB 258 TACTGCCGAGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 317  
QY 1144 TGACATACCTGACATGATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1186  
DB 318 GGATGTGCCAGATATGATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 360

RESULT 14  
US-08-765-662-13  
Sequence 13, Application US/08765662  
Patent No. 5929213  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,662  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 536  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745  
FILING DATE: 12-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Ph.D., Lisa A  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2419 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 218..1267  
OTHER INFORMATION:  
US-08-765-662-13

Query Match  
Best Local Similarity 65.3%; Pred. No. 3,6e-26;  
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;

QY 844 CTGCCAAGGAGGCTCCAGATGCTGTCGACAGATTGTTTGGACTCCGTAGAT 903  
DB 934 CTGTGAGGCTCGAGACCCCTTATGTCAGGCGAGACATTAAGTACACTCCAGGAAC 993  
QY 904 TGGCTGGACAGACTGATATCAGCCTGAGGGCTACGCCATGAATTTGCTAGGCA 963  
DB 994 GGGATGGGAGGAGTGGATACAGCCGAGGGGATACAGCAATTAATGCTGAGTGGCA 1053  
QY 964 GTGCCACTACATAGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023  
DB 1054 GTGCCCTCCCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113  
QY 1024 CAATCTTCAAGGCCACACAGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 1083  
DB 1114 CAGCTCTCTCAAGGCCACACATCT-----TGGCTGCAAGTACCTCTGCTGCTGCT 1167  
QY 1084 CAGGCGCGGCGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
DB 1168 TACTGCCGAGAGGCGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1227  
QY 1144 TGACATACCTGACATGATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1186  
DB 1228 GGATGTGCCAGATATGATGATGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCT 1270

RESULT 15  
PCT-US95-08745-13  
Sequence 13, Application PC/TUS9508745  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla

STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745  
FILING DATE: 12-JUL-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hall, Ph.D., Lisa A  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2419 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 218...1267  
OTHER INFORMATION:  
PCT-US95-08745-13

Query Match 6.2%; Score 140.2; DB 5; Length 2419;  
Best Local Similarity 65.3%; Pred. No. 3.6e-26;  
Matches 224; Conservative 0; Mismatches 113; Indels 6; Gaps 1;  
QY 844 CTGCCAAGAGAGGAGTGTGCTGCTGAGACAGTTTGTGACTTCCCTGAGAT 903  
DB 934 CTGTGAGGCTCGGACCCCTTATGTGCGAGCGAGACCATTAAGTCCAGGAACT 993  
QY 904 TGCGTGGCAGCAGCTGATCATCCAGCTGAGGCTACGCCATGAATTCATGATAGGGA 963  
DB 994 GCGATGGGGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053  
QY 964 GTGCCACTACATAGCAGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1023  
DB 1054 GTGCCCTCCCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1113  
QY 1024 CAATCTTCTCAAGGCAACACAGCTGCAAGGCACTGAGGGGCTCATGCTGTGACT 1083  
DB 1114 CAGCTCTCTCAAGGCAACACATCTT-----TGGCTTGCACATGCTGCTGCTGCTGCT 1167  
QY 1084 CAGGGCCCGGGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1143  
DB 1168 TACTGCCCGAAGGCGCCCT 1227  
QY 1144 TGACATACCTGACATGAGTAGAGAGGCTGTGGGTGCACTTAG 1186  
DB 1228 GGAATGTGCAATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1270

Search completed: October 11, 2002, 22:15:16  
Job time: 64.7958 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 22:15:08 : Search time 1835.4 Seconds  
(without alignments)  
16707.608 Million cell updates/sec

Title: US-09-684-383-1

Perfect score: 2272  
Sequence: 1 CAGCAGCCATCCAGCTCG.....ACTATGATCATCTCTCTT 2272

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Database :

EST.\*  
1: em\_estdb.\*  
2: em\_esthm.\*  
3: em\_estln.\*  
4: em\_estnu.\*  
5: em\_estpl.\*  
6: em\_estro.\*  
7: em\_estro.\*  
8: em\_estro.\*  
9: gb\_estl.\*  
10: gb\_estl.\*  
11: gb\_estl.\*  
12: gb\_estl.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	738.2	32.5	1011 11	BC020693 Homo sapi
2	499.4	22.0	541 10	BC020693 Homo sapi
3	418	18.4	758 10	BC020693 Homo sapi
4	416.8	18.3	893 10	BC020693 Homo sapi
5	404.8	17.8	829 10	BC020693 Homo sapi
6	401.2	17.7	823 10	BC020693 Homo sapi
7	399	17.6	841 10	BC020693 Homo sapi
8	396	17.4	841 10	BC020693 Homo sapi
9	378	16.6	816 10	BC020693 Homo sapi
10	369.2	16.2	975 10	BC020693 Homo sapi
11	283.2	12.5	594 9	AV658436 AV658436
12	283.2	12.5	1113 10	BM463852 AGENCOURT
13	281.4	12.4	475 10	BM463852 AGENCOURT
14	280	12.3	589 10	BM463852 AGENCOURT
15	279.4	12.3	567 10	BM463852 AGENCOURT
16	279	12.3	329 10	BM463852 AGENCOURT
17	279	12.3	359 10	BM463852 AGENCOURT

18	279	12.3	404 10	BE852372 UN19606.x
19	279	12.3	440 10	BE996475 UT-M-CGP
20	279	12.3	644 10	BE996475 UT-M-CGP
21	278.4	12.3	585 12	AZ795923 2M0051H22
22	276.4	12.2	420 10	BE662934 602144726
23	276.4	12.2	513 10	BE996475 UT-M-CGP
24	276	12.1	376 10	BE996475 UT-M-CGP
25	276	12.1	568 10	BE996475 UT-M-CGP
26	275.8	12.1	346 9	BE133911 uq06e07.x
27	275	12.1	506 10	BE996475 UT-M-CGP
28	274	12.1	347 9	AA620486 ae60b02.s
29	273.4	12.0	537 10	BE996475 UT-M-CGP
30	273	12.0	522 9	AI954151 wx80d04.x
31	272.8	12.0	549 9	AI954151 wx80d04.x
32	272.4	12.0	566 9	AM209153 uq02f01.x
33	272.2	12.0	475 10	BE996475 UT-M-CGP
34	271.4	11.9	443 9	AI201615 qb81c01.x
35	268	11.8	479 9	AA029894 zk08f02.s
36	268	11.8	631 10	BM272210 1440f09.x
37	267	11.8	285 9	AA183246 mt82g07.r
38	267	11.8	443 10	BE109198 7158b11.x
39	267	11.8	538 10	BE684212 602141120
40	266.4	11.7	358 9	AA011197 ze23c01.s
41	266.4	11.7	603 9	AU143968 AU143968
42	266	11.7	348 9	AM268442 xv40b05.x
43	266	11.7	714 10	BI861129 603390870
44	265.4	11.7	583 9	AA877215 ob15e02.s

## ALIGNMENTS

RESULT 1  
LOCUS BC020693  
DEFINITION Homo sapiens, similar to inhibin, beta C, clone IMAGE:4723762,  
mRNA.  
ACCESSION BC020693.1 GI:18088855  
VERSION BC020693.1  
KEYWORDS HNC  
SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 1011)  
AUTHORS Strausberg, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2002) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT  
Contact: MGC help desk  
Email: gcapbs-remail.nih.gov  
Tissue Procurement: CLONTECH  
CDNA Library Preparation: CLONTECH Laboratories, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) mcdpax11.stanford.edu  
Dickson, M., Schmutz, J., Gilwood, J., Rodriguez, A., and Myers,  
R. M.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 37 Row: 9 Column: 11  
This clone was selected for full length sequencing because it  
passed the following selection criteria: matched mRNA gl: 15718678  
This clone has the following problem: frame shifted.  
Location/Qualifiers  
1..1011



QY	420	TCATCAGCTTTGGTGGAGAGAGGCGCTCCACATCACCAGACCTGCTTGATTTTCACT	479
Db	437	TCATCAGCTTTGGTGGAGAGAGGCGCTCCACATCACCAGACCTGCTTGATTTTCACT	496
QY	480	TCTCCCTGATAGACAGCTGCTGAGACAGGAGAGTCCAGCAGGCCA	524
Db	497	TCTCCCTGATAGACAGCTGCTGAGACAGGAGAGTCCAGCAGGCCA	541
RESULT 3			
LOCUS	BI328115	758 bp	MRNA
DEFINITION	602979264F1 NCI_CGAP_L19	Mus musculus	cDNA clone IMAGE:5132391 5'
ACCESSION	BI328115		
VERSION	BI328115.1	GI:15012772	
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus-		
TITLE	1 (bases 1 to 758)		
JOURNAL	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: <a href="mailto:cgaps-f@mail.nih.gov">cgaps-f@mail.nih.gov</a>		
	Tissue Procurement: Jeffrey E. Green, M.D.		
	cDNA Library Preparation: Life Technologies, Inc.		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	<a href="http://image.llnl.gov">http://image.llnl.gov</a>		
	Plate: LLAM1324 row: 0 column: 16		
	High quality sequence stop: 758.		
FEATURES	Location/Qualifiers		
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	/strain="FVB/N"		
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	/clone="IMAGE:5132391"		
	/clone_1lb="NCI_CGAP_L19"		
	/lab_host="DH10B (T1 phage-resistant)"		
	/note="Organ: liver; Vector: pCMV-SPORT6; Site_1: NotI;		
	Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.		
	Average insert size 1.9 kb. Constructed by Life		
	Technologies. Note: this is a NCI_CGAP library."		
BASE COUNT	168 a 229 c 194 g 167 t		
ORIGIN			
Query Match	18.4%;	Score 418;	DB 10; Length 758;
Best Local Similarity	75.9%;	Pred. No. 1,9e-55;	
Matches 557; Conservative	0; Mismatches 170; Indels 7; Gaps 3		
QY	35	AGGGCGCTGCGAGCGACAGAGAGTTGGAGACCACTGTTGAGACCTGAGCCCTGAG	95
Db	1	AGGGCTCCCTGGCGCCAGACAGAGTTGAGACCACTCCCGTTGAGACCTGATATAGGC	60
QY	96	TCTGATATGCTCAAGAAGGCGCTTCCCAACAATGACCTCTCATTTGCTTGGGCTTTC	195
Db	61	TTTGGGCTCTTTAAGAGGCTATCTCCACGAATGGCTCTCTCTTGGCTCGGGCTCTTC	120
QY	156	TCTCTCCTGCTCCAGACAGAGTGCGCCACTCCAGAGCTGCGGCTCAGTGTCCAGCATGTG	215
Db	121	TGTTCTCTGACCTCAACACAGTAGTGAACCCAAAGCTGAGGCTCATGCGCAGCATGTT	180
QY	216	GGGGGCGCCACTTTGGAACTTGAGAGCGAGGGAGGCTCTTCTGATCTGGCCAGAGAGA	275
Db	181	GGCGTGCCTTTTGGACCTTGAGAGCGAGGGGAGCTCTCTCGATTTTGGCCAAAGAAA	240
QY	276	GCATCTTGACAAAGCGACCTCACCAGGCGCCCAACGCTGAACCGCCCTGTGTCCAGAG	335

D	b	241	GTAATCCGACAAAGCTGCACCTCAGCCAGCGCCCCCAATACGTAGTGGCCAGTGTCACAG	300
O	y	336	CTGCTTTGAGGACATCGACTCGAGACCCTCACGGGGTCCCACAGGGGCACTTAGAG-	394
D	b	301	GGGCTCTAACAGACCGCGCTTCCGCCGGCCCTCGACAGGGAAACCTGTGGAGC	360
O	y	395	--GACACAGGGAACAGGAATGTCAATCATCAGCTTTTGCTGAGACAGAGCCTCTCCACA	452
D	b	361	AYGACACAGGACAGAAMAATATGGAATCATCAGCTTTGCTGACACAGACCTCTCACCA	420
O	y	453	TCAAACGACCTGCTTGTATTTCATCTCTCTGTGATAGAACTGCTGGTGACAGAGAG	512
D	b	421	TCAACACACCCGGGTGAGTTCACCT--CTGTGTAATATGGCCAGATGGCATGAGAG	477
O	y	513	TCCACAGCGCCAGTCTCATGTTCTTTGGACAGCTCCCTTCCAAATACCACTTGGACCTTGA	572
D	b	478	TCCGCGAACCOCCTTCAATGTTCTTCTGTCAGTGTCCCCACAAATGCAACCCAGACATGA	537
O	y	573	AAGTAGAGTCCCTTGTGCTGGGTCCACATAATACCAACCTCACTTGGCTACTAGTACC	632
D	b	538	ATATAGAGTTCTTGTGTAAGACATATGACACCAACCTCACTTGAACAAGTACGTACG	597
O	y	633	TGCTGAGAGTGATGCCAGTGGCTGGCATCAACCTCCCTTAGGCTGTAAAGTCAAGCTG	692
D	b	598	TGTGTAGGTGTAATGCCAGTGGCTGGTACCAACCTTCTCTGGAGCTTGAACTCAAGCT	657
O	y	693	CCTGCAGCCAGGAGGACCTGACCTCTGGAGCTGTACTTCT--AAGGCGAGGTAGCCAGAC	751
D	b	658	CTTGGAGCCAGGACCACTTACTCTGGAGCTGTACACAGAAAACCAATGTGGCCACAGT	717
O	y	752	TCAGTCATCTGGG	765
D	b	718	TCCTTGATCTGGG	731
		RESULT 4		
		B1246740	893 bp mRNA linear EST 17-JUL-2000	
		LOCUS	602959660E1 NCI_CGAP_L19 Mus musculus cDNA clone IMAGE:5125287 5'	
		DEFINITION	mRNA sequence.	
		BI246740		
		ACCESSION	B1246740.1 GI:1479095	
		VERSION		
		KEYWORDS	EST.	
		SOURCE	house mouse.	
		ORGANISM	Mus musculus	
		REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
		AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
		TITLE	NIH-MGC http://mgc.nci.nih.gov/	
		JOURNAL	1 (bases 1 to 893)	
		COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC)	
			Unpublished (1999)	
			Contact: Robert Strausberg, Ph.D.	
			Email: cgapbs-r@mail.nih.gov	
			Tissue Procurement: Jeffrey E. Green, M.D.	
			cDNA Library Preparation: Life Technologies, Inc.	
			CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	
			DNA sequencing by: Incyte Genomics, Inc.	
			Clone distribution: MGC clone distribution information can be	
			found through the I.M.A.G.E. Consortium/LLNL at:	
			http://image.llnl.gov	
			Plate: LMAM1306 row: g column: 16	
			High quality sequence stop: 778.	
			Location/Qualifiers	
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			/clone_1ib="IMAGE:5125287"	
			/lab_host="DH10B (r1 phage-resistant)"	
			/note="Sali; Vector: pCMV-Sport6; Site.1: NotI;	
			Site.2: SalI; Cloned unidirectionally. Primer: Oligo dT.	
			Average insert size 1.9 kb. Constructed by Life	

Technologies. Note: this is a NCI\_CGAP Library.  
 BASE COUNT 196 a 259 c 242 g 196 l  
 ORIGIN

Query Match 18.3%; Score 416.8; DB 10; Length 893;  
 Best Local Similarity 74.7%; Pred. No. 2,7e-55;  
 Matches 644; Conservative 0; Mismatches 202; Indels 16; Gaps 9;

OY 96 TCTGATGCTCAAGAGAGGCTTCCCAACATGACCTCTCTTCTGCTGCTTC 155  
 DB 5 TTTGGGCTCTTAAAGAGCTATCTCCACAAATGGCTCTCTCTGCTGCTTC 64  
 OY 156 TCCCTGCTGCTCAACAGAGTGGCCATCCAGAGTGGCGGTCTGCTGCTGCTG 215  
 DB 65 TCTTCTGCTCAACAGAGTGGCCATCCAGAGTGGCGGTCTGCTGCTGCTG 124  
 OY 216 GGGGCCCCACCTTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 275  
 DB 125 GGGGCGCATCTTTGACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 184  
 OY 276 GCATCTTGAAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 335  
 DB 185 GTATCTGAGAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 244  
 OY 336 CTGCTTGAAGAGTGAAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 394  
 DB 245 GGGGCTCAAG 304  
 OY 395 --GACACAG 452  
 DB 305 ATGACACAG 364  
 OY 453 TCAACAG 512  
 DB 365 TCAACAG 422  
 OY 513 TCCAG 572  
 DB 423 TCCAG 482  
 OY 573 AAGTGAAG 632  
 DB 483 ATATGAAG 542  
 OY 633 T-GCTGAG 691  
 DB 543 TGGTGAAG 602  
 OY 692 GCGTGAAG 749  
 DB 603 GCGTGAAG 662  
 OY 750 GCTGAG 809  
 DB 663 GTTCTGAG 722  
 OY 810 GGGG----CAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 863  
 DB 723 GAGGAG 782  
 OY 864 -TGTGCTGAG 921  
 DB 783 TTTGCTGAG 842  
 OY 922 CATGAG 943  
 DB 843 CATGAG 864

RESULT 5  
 LOCUS B1329959 829 bp mRNA linear EST 30-JUL-2001  
 DEFINITION 60280519F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5133317 5'

ACCESSION mRNA sequence.  
 B1329959  
 VERSION B1329959.1 GI:15014616  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE NIH-MGC http://mgc.nci.nih.gov/.  
 AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
 TITLE Unpublished (1999)  
 JOURNAL Contact: Robert Strausberg, Ph.D.  
 COMMENT Email: cgabs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNLN at:  
 http://image.lnl.gov  
 Plate: LLM11327 row: f column: 06  
 High quality sequence stop: 789.

FEATURES  
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 /organism="Mus musculus"  
 /strain="FVB/N"  
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 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: Liver; Vector: pCMV-Sport6; Site\_1: NCI; Site\_2: Sall; Cloned unidirectionally; Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP Library."

BASE COUNT 187 a 246 c 217 g 179 t  
 ORIGIN

Query Match 17.8%; Score 404.8; DB 10; Length 829;  
 Best Local Similarity 74.9%; Pred. No. 2e-53;  
 Matches 574; Conservative 0; Mismatches 182; Indels 10; Gaps 5;

OY 24 CACACTTCTCCAG 83  
 DB 49 CACACTTCTCCAG 108  
 OY 84 CTGAG 143  
 DB 109 CTGAGATATAG 168  
 OY 144 TTTGAG 203  
 DB 169 TCTGAG 228  
 OY 204 GTGAG 263  
 DB 229 GCGGAG 288  
 OY 264 TGGCAAG 323  
 DB 289 TGGCAAG 348  
 OY 324 CTGTGCTGAG 383  
 DB 349 CAGTGTGAG 408  
 OY 384 CACTTCTAGAG--GACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 440  
 DB 409 CCTGTAG 468  
 OY 441 GCGTCTCCACATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 500  
 DB 469 ACCTCTCCACATCAACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 525

QY 501 GTGACAGGAGGTCACAGGCGACGTCATGTTCTTTGTGACGCTCCCTCCAAATACCA 560  
 DB 526 GTGGCATGAGAGGTCGCGAGAGCCGCTTCATGTTCTTGTGAGAGTCCCGCCAAATGCA 585  
 QY 561 CTGGACCTTGAAGATGAGTACCTCTTGTGCTGGGTCCACATTAATACCAACGCTACCTTGG 620  
 DB 586 CCCGACCATTAATATAGATTTCTTGTGCTAAGACCATATGACAGCAAT-CTCACCTTGA 644  
 QY 621 CTACTGACATCTCTGAGGTGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680  
 DB 645 CAATGACATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 703  
 QY 681 AAGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 740  
 DB 704 AAGCTCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 761  
 QY 741 TAGCCACAGCTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 786  
 DB 762 GTGGCCACAGTACCTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 807  
  
 RESULT 6  
 BF533960 823 bp mRNA linear EST 11-DEC-2000  
 LOCUS 602075120P1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4212125 5'  
 DEFINITION  
 mRNA sequence.  
 ACCESSION BF533960  
 VERSION BF533960.1 GI:11621323  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 823)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM49782 row: 9 column: 06  
 High quality sequence stop: 754.  
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 /organism="Mus musculus"  
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 /lab\_host="DH10B (TI phage-resistant)"  
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 Site\_2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 181 a 247 c 221 g 174 t  
 ORIGIN  
 Query Match 17.7%; Score 401.2; DB 10; Length 823;  
 Best Local Similarity 75.3%; Pred. No. 7.2e-53;  
 Matches 593; Conservative 0; Mismatches 183; Indels 12; Gaps 7;  
 QY 43 CTGGACAGGAGGTCACAGGCGACGTCATGTTCTTTGTGACGCTCCCTCCAAATACCA 102  
 DB 5 CTGGTCCGACAGGAGGTCACAGGCGACGTCATGTTCTTTGTGACGCTCCCTCCAAATACCA 63  
 QY 103 TGCTCAAGAGGCTTCCGACGATGACCTTCATGCTTGTGCTTCTCTCTCT 162

DB 64 CTTTAAAGAGGCTATCTCTCAGCATATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 123  
 QY 163 GGCTCAACACCACTGAGCCACTCCAGAGCTGGGTCAGTGTGCTCAGATGTGGGGGCC 222  
 DB 124 GACTCCAAACCACTACTGAAACCCCAAAACTGAGGGTCAATGCCCATGTTGGGCTGC 183  
 QY 223 CACCTTGAAGTGAAGAGCCAGCGGAGAGCTGCTTCTATCTGCGCAAGAAAGATCTT 282  
 DB 184 CATCTTGACCTGGAAGAGCCAGCGGAGAGCTGCTTCTCAT-TGGCCAAAGAAAGATCTT 242  
 QY 283 GGAAAGCTGAGCTCCACCCAGCGGCCCAACACTGAACGCCCTGTGCTCAGAGCTCTT 342  
 DB 243 GGAAAGCTGAGCTCCAGCGGCCCAACACTGAACGCCCTGTGCTCAGAGCTCTT 302  
 QY 343 GAGAGCTGACCTGAGCAGCTCCAGCGGGTCCACAGAGGGGACCTTGTAGAG--GACAA 399  
 DB 303 CAAGACCCGCTGAGCGGCTCCGCGGCTGAGCGGAAACCTTGTGACATGACCA 362  
 QY 400 CAGGAGACAGAAATGTGAATCATCAGCTTCTGAGACAGGCTCTCCACATCAACCA 459  
 DB 363 GAGACAAAGAAATGTGAATCATCAGCTTCTGAGACAGGCTCTCCAGATCAACCA 422  
 QY 460 GACTGCTCTGATTTTCACTTCTCTCTGATGAACTGCTGAGACAGGAGTCCAGCA 519  
 DB 423 GACCCGCTGAGTTCACCTT--CTGTGTGAATGAGCCAGTGGATGAGTCCGGCA 479  
 QY 520 GGGCAGCTCATGTTCTTGTGCTCAGAGCTCCCTTCCAAATACCACTTGTGAGTGAAGTGA 579  
 DB 480 GACCCGCTTCACTTCTTGTGCTCAGAGTCCCGCCAAATGACACCATGTAATTAAG 539  
 QY 580 AGTCTTGTGCTGGGTCCACATTAATCAAA--CCTACCTTGGCTTACTGATCTGCTG 637  
 DB 540 AGTCTTGTGCTGAGACATATGACACCAAACTCACCCTTGCACAGTCACTGCTGCTG 599  
 QY 638 GAGGTGATGCCAGTGGCTGCGATCAACCTCCCTGAGGCTCAAGCTCAAGTCTGCTG 697  
 DB 600 CAGGTGAATGCCAGTGGTGTGACAGCTTCTCTGAGCTCAAGCTCAAGCTGCTGCTG 658  
 QY 698 AGCCAGGAGCAGCTGACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 757  
 DB 659 AGCCAGGATACCTTACTGCTGAGCTGTGACAGAAACCCAGGAGCCACAGTCTTGT 718  
 QY 758 ATCTGAGTGGAGCTGCTCCATAGGCTTGTGCTGAGCCCGGCTGAGAGTGGGGGCA 817  
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 QY 818 CACCATAT 825  
 DB 778 CTCCGGTT 785  
  
 RESULT 7  
 B1145698 841 bp mRNA linear EST 05-JUL-2001  
 LOCUS 602909844F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5050810 5'  
 DEFINITION  
 mRNA sequence.  
 ACCESSION B1145698  
 VERSION B1145698.1 GI:14605699  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;  
 1 (bases 1 to 841)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 COMMENT





Db 479 CAGCAACATTGTCAGACGATATACCTGACATGCTGCTGAGGCTGCGGGCTGATCTTA 538  
 Oy 1186 GTCTATGTGTGATGGGACAGCCCAAGTTGATGG 1221  
 Db 539 GCTTATGGGTGATACAGGCTGCTGAGGTAGATGG 574

RESULT 9  
 BF232704 816 bp mRNA linear EST 14-NOV-2000  
 LOCUS 602023292F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4158766 5'  
 DEFINITION mRNA sequence.  
 ACCESSION BF232704  
 VERSION BF232704.1 GI:11142342  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgc.nci.nih.gov/  
 1 (bases 1 to 816)  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 CDNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LAM9435 row: 9 column: 23  
 high quality sequence stop: 714.  
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 /organism="Mus musculus"  
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 /note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; NCI;  
 Site\_2: Salt; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 167 a 253 c 221 g 175 t

Query Match 16.6% Score 378; DB 10; Length 816;  
 Best Local Similarity 74.5%; Pred. No. 2.8e-49;  
 Matches 556; Conservative 0; Mismatches 180; Indels 10; Gaps 6;

Oy 29 TTTCTCCAGGGGCTCTGCAGACGAGAGTGTGAGACACAGCTGTGAGACCCCTGAG 88  
 Db 7 TTCTCCAGGGGCTCTGTGAGAGAGAGTGTGAGACACAGCTGTGAGACCCCTGAA 66  
 Oy 89 CCTGTAGTCTGATTTGCTCAAGAGGGCTTCCCAAGATGACTCTGATTTGCTGTG 148  
 Db 67 TATAGGCT-TGGGTCTCTTAAGAGAGGCTATCTCCAGCATGCGCTTCTGCTCTG 125  
 Oy 149 GCGTTTCTCTCTGCTGCTCAACACAGTGGCCACTTCCCAAGACTGGCGGTCACTGCCA 208  
 Db 126 GCTCTCTGCTCTGCTGCTCAACACAGTGTGAGACCCCAAACTGAGGCTCCATGCCCA 185  
 Oy 209 GCATGTGGGGGGCCACCTTGTGAGAGAGGAGGAGGAGGAGCTTGTGATTTGGCC 268  
 Db 186 GCATGTGGGGGGCCATTTTGTGAGAGAGGAGGAGGAGGAGGAGGAGTGTGATTTGGCC 245  
 Oy 269 AAGAGAGCATTTGAGCAAGCTGACCTCACCGAGGCGCCCAACTGAACCGCCCTGTG 328  
 Db 246 AAGAAAGATCTCTGCAACAGCTGACCTGAGCGAGCGCCCATATCTCACTGCGGCAAGTG 305

Oy 329 TCCAGAGCTGCTTTGAGAGCTGACCTGACAGCTCCAGCGGGGTCGCCAAGGGGCACTT 388  
 Db 306 TCCAGAGGGGCTCTCAAGAGCCGCGCTGACAGCGCTCGCGGGCTCCAGGGGAACCTTG 365  
 Oy 389 CTAGAG---GACAACAGAGGAACAGAGATGTGAAATCATCAGCTTTGTGACAGAGGCTG 445  
 Db 366 TTGGAGCATGACAGAGACAGAGAGATATGAGATCATCAGCTTTGTGACAGAGACTG 425  
 Oy 446 TCCAGCATCAACAGAGAGCTGCTTTGATTTTCTGCTCTGTATAGAACTGCTGTTGAC 505  
 Db 426 TCCAGAGATCAACAGAGAGCCGCTGAGTTCACACT---CTCTGTGTAATGAGCCAGTGGC 482  
 Oy 506 AGGAGGTCCAGAGAGGCTGATCTTCTTTTGTGAGAGCTCCCTTCCAAATACACATTGG 565  
 Db 483 ATGAGAGTCCGAGAGAGAGCCCTTCATGTTCTGTGAGAGTCCCAAAATGACACCCAG 542  
 Oy 566 ACCGTAAAGTGAAGAGAGCTGCTGCTGCTGATATACCACTTCACTTGGCTACT 625  
 Db 543 ACCATGATATTAAGAGTTCTTGTCTAAGACCATATGACACCAATACCTTGGACAGT 602  
 Oy 626 CAGTACTGCTGAGAGTGTGATGCCAGTGGCTGAGCATCTCCCTTAGGCGCTGAGC- 684  
 Db 603 CAGTACTGCTGAGAGTGTGATGCCAGTGGCTGAGCATCTCTCTGAGCTGAGC- 662  
 Oy 685 TCAAGCTGCTGCA-GCCAGGGGCACTGAC-CCTGAGAGCTGTACTTGAAGGCCAGGTA 742  
 Db 663 TCAAGCTGTTTGCAGGCGAGGACACCTTACTCTGTGAGCTGTGATCCGAAAGCCGTTG 722  
 Oy 743 GCCCAGAGCTCAGTCATCTGCGGTGG 768  
 Db 723 GCCCAGCTCTGTGATCCCGGGGTGG 748

RESULT 10  
 BF533968 975 bp mRNA linear EST 11-DEC-2000  
 LOCUS 602075129F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4212175 5'  
 DEFINITION mRNA sequence.  
 ACCESSION BF533968  
 VERSION BF533968.1 GI:11621331  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NIH-MGC http://mgc.nci.nih.gov/  
 1 (bases 1 to 975)  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgaps-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 CDNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LAM9782 row: 1 column: 08  
 high quality sequence stop: 659.  
 Location/Qualifiers  
 1..975  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone\_image="4212175"  
 /clone\_id="NCI\_CGAP\_L19"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; NCI;  
 Site\_2: Salt; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCI\_CGAP Library."  
 BASE COUNT 190 a 297 c 266 g 222 t

## ORIGIN

Query Match 16.2%; Score 369.2; DB 10; Length 975;  
 Best Local Similarity 75.3%; Pred. No. 6e-48;  
 Matches 527; Conservative 0; Mismatches 163; Indels 10; Gaps 5;

96 TCTGATTCCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 155  
 3 TTTGGGCTCTTAAGAGAGGCTATCTCCACCAATGGCTCTCTCTGCTGCTTTC 62  
 156 TCTCTGCTGCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 215  
 63 TGTTCCTGCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 122  
 216 GGGGGGCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 275  
 123 GGGGGGCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 182  
 276 GCATCTTGGAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 334  
 183 GTATCTTGGAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 242  
 335 GCTGCTTGGAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 394  
 243 GGGGGGCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 302  
 395 ---GACAAAGAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 451  
 303 CATGACCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 362  
 452 ATCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 511  
 363 ATCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 419  
 512 GTCCAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 571  
 420 GTCCAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 479  
 572 AAGTGAAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 631  
 480 AATATAAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 539  
 632 CTGCTGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 690  
 540 GTGCTGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 599  
 691 TGCTGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 750  
 600 TGCTGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 750  
 751 CTGAGTATCTCTGCTGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 790  
 658 GTTCTGATCTCTGCTGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 697

RESULT 11  
 AV658436 594 bp mRNA linear EST 16-JAN-2002  
 AV658436 GLC Homo sapiens cDNA clone G1CFME02 3', mRNA sequence.

AV658436  
 DEFINITION  
 AV658436  
 AV658436  
 AV658436.1 GI:9879450  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 AUTHORS  
 Xue, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.,  
 Xiao, H., Qu, J., Liu, F., Huang, Q., Cheng, Z., Li, N., Du, J., Hu, W.,  
 Shen, K., Lu, G., Fu, G., Zhong, M., Xu, S., Gu, W., Huang, W., Zhao, X.,  
 Hu, G., Gu, J., Chen, Z., and Han, Z.  
 Insight into hepatocellular carcinogenesis at transcriptome level  
 by comparing gene expression profiles of hepatocellular carcinoma

JOURNAL  
 MEDLINE  
 COMMENT  
 with those of corresponding noncancerous liver  
 Proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)  
 21625106  
 Contact: Zengqiang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex. 45)  
 Fax: 86-21-50801922  
 Email: hanzg@hgsc.sh.cn  
 This clone is available at CHCC in Shanghai.

## FEATURES

source

Location/Qualifiers

1..594

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="G1CFME02"

/clone\_id="GLC"

/tissue\_type="corresponding non cancerous liver tissue"

/dev\_stage="Adult"

/lab\_host="SOLR"

/note="Vector: pBluescript sk(-); Site\_1: EcoRI; Site\_2: XhoI"

BASE COUNT 179 a 126 c 123 g 166 t

## ORIGIN

Query Match 12.5%; Score 283.2; DB 9; Length 594;  
 Best Local Similarity 99.0%; Pred. No. 1.5e-34;  
 Matches 285; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

96 TCTGATTCCTCAAGAGAGGCTTCCACCATGACCTCTCTCATTTGCTTGGCTTTC 2044  
 3 TTTGGGCTCTTAAGAGAGGCTATCTCCACCAATGGCTCTCTCTGCTGCTTTC 297  
 2045 GGTACCACTACCAATTTACAGGCAATATCTGATGTAATGAAGAAAGAA 2104  
 296 GGTACCACTACCAATTTACAGGCAATATCTGATGTAATGAAGAAAGAA 237  
 2105 GACAAAGCTACCAATTTACAGGCAATATCTGATGTAATGAAGAAAGAA 2164  
 236 GACAAAGCTACCAATTTACAGGCAATATCTGATGTAATGAAGAAAGAA 177  
 2165 TTAATCAATAGCTGACTTTTGAACAGTGGCTATGACAGTCTGAAAGAGGCT 2224  
 176 TTAATCAATAGCTGACTTTTGAACAGTGGCTATGACAGTCTGAAAGAGGCT 117  
 2225 TCTGTTTAAAGCTGACGTAATCTTGTGACTAGTATGATGCTTCCCT 2272  
 116 TCTGTTTAAAGCTGACGTAATCTTGTGACTAGTATGATGCTTCCCT 69

RESULT 12  
 BM463852 1113 bp mRNA linear EST 05-FEB-2002  
 AGENCOURT\_6445395 NIH\_MGC\_72 Homo sapiens cDNA clone IMAGE:5539850  
 5', mRNA sequence.

BM463852  
 DEFINITION  
 BM463852  
 BM463852  
 BM463852.1 GI:16512894  
 EST.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 AUTHORS  
 NIH-MGC http://mhc.nhl.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cga@pds-remail.nih.gov  
 Tissue Procurement: ATCC/DCID/DTF  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be





GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 11, 2002, 22:15:33 : Search time 41 Seconds  
(without alignments)  
953.609 Million cell updates/sec

Title: US-09-684-383-2

Perfect score: 1849  
Sequence: 1 MRSLLLAFLAFLAFTVATP.....DSNVKTDIPDMVEACGCS 352

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:\*  
2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:\*  
3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:\*  
4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:\*  
5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:\*  
6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:\*  
7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:\*  
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22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	1849	100.0	352 17	Transforming growth
2	1838	99.4	352 22	Human TGF-beta MFI
3	1392	75.3	352 19	Murine liver Actin
4	664	35.9	350 17	Human growth diffe
5	664	35.9	350 22	Human polypeptide
6	655	35.4	350 19	Human liver actin
7	648	35.0	350 19	Murine liver actin
8	599.5	32.4	407 21	Human inhibin B be
9	599.5	32.4	407 21	Human activin B su
10	590	31.9	353 8	Sequence of human
11	578	31.3	351 8	Sequence of porcine

12	558.5	30.2	427 8	AA1970200
13	557	30.1	426 8	AA1970203
14	557	30.1	426 21	AA192016
15	557	30.1	426 21	AA192018
16	555	30.0	426 11	AA195413
17	469	25.4	87 14	AA195447
18	444	24.0	127 12	AA19091
19	439.5	23.8	303 22	AA192908
20	422	22.8	288 7	AA190518
21	388.5	21.0	121 22	AA193203
22	375	20.3	122 22	AA193202
23	373	20.2	130 7	AA190520
24	369.5	20.0	115 13	AA196482
25	368.5	19.9	115 13	AA195129
26	368.5	19.9	115 13	AA195123
27	368.5	19.9	116 13	AA195127
28	366.5	19.8	115 8	AA191197
29	366.5	19.8	115 8	AA191177
30	366.5	19.8	115 11	AA1908216
31	361.5	19.6	115 9	AA190820
32	360	19.5	116 13	AA196481
33	358	19.4	116 11	AA1905444
34	357	19.3	116 8	AA191196
35	357	19.3	116 8	AA191176
36	357	19.3	116 9	AA1908019
37	357	19.3	116 9	AA192061
38	357	19.3	116 11	AA1905443
39	357	19.3	116 11	AA1908215
40	357	19.3	116 13	AA1925128
41	357	19.3	116 14	AA191622
42	357	19.3	116 21	AA1967949
43	354	19.1	116 12	AA192088
44	353	19.1	130 12	AA190990
45	345	18.7	116 9	AA191906

## ALIGNMENTS

RESULT 1  
ID AAR89729 standard: Protein; 352 AA.  
AC AAR89729;  
DT 09-AUG-1996 (first entry)  
XX  
XX  
DE Transforming growth factor beta MP-121.  
KW TGF-beta; MP-121; mitogen; differentiation; induction; promotion;  
KW maintenance; morphogen; tissue regeneration; dental implantation;  
KW wound healing.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
FH Key location/Qualifiers  
FT Protein 237..352  
FT /label= mature\_protein  
XX  
XX DE19511243-A1.  
XX  
XX PD 04-JAN-1996.  
XX  
XX PF 27-MAR-1995. 95DE-1011243.  
XX  
XX PR 01-JUL-1994. 94DE-1423190.  
XX  
XX PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
XX Bechtold R, Neidhardt H, Pohl J, Hoettgen G;  
XX MPI; 1996-050788/06.  
XX N-PSDB; AAT11104.

Sequence of porcine  
Sequence of human  
Human inhibin A be  
Human activin A su  
TGF-beta human differ  
TGF-beta-like clon  
Xenopus Bone Morph  
Angiotensin conver  
Sequence of bovine  
Inhibin betaab C-t  
Inhibin betaab C-t  
Sequence of human  
Activin-like pepti  
Human KRN-5M, Hom  
BUF-4, Synthetic.  
Activin B, Synth  
Sequence of verteb  
Second protein cha  
Follicle stimulat  
Sequence of the 14  
Activin-like pepti  
Monomer B of BUF-4  
Sequence of verteb  
Second protein cha  
Sequence of the 14  
Polypeptide BUF-3  
Monomer A of BUF-4  
Follicle stimulat  
Activin AB, Synth  
BUF-3, Synthetic.  
Human activin A SE  
16.5 kD subunit of  
Xenopus Bone Morph  
N-terminal of Inhl

XX DNA encoding transforming growth factor beta MP-121 - has mitogenic  
 PT and differentiation-inducing activity, e.g. for use in wound healing  
 XX  
 PS Claim 7; page 11; 15pp; German.

CC A cDNA library prepared using total RNA from human liver was  
 CC subjected to PCR amplification using primers corresp. to conserved  
 CC regions within the TGF-beta family. Amplification products were  
 CC subcloned and sequenced. One clone (designated PSK-MP121) was found  
 CC to contain a new sequence. Part of the insert from the clone was  
 CC used to re-screen the human liver cDNA library and a 2272 bp fragment  
 CC coding for a TGF-beta-like protein (i.e. the present sequence) was  
 CC isolated. This protein has mitogenic and differentiation-inducing  
 CC properties making it (or fusion proteins comprising it or heterodimers  
 CC of the protein with a cysteine knot motif protein) useful for inducing  
 CC tissue regeneration, e.g. for wound healing, inducing growth of  
 CC hepatic tissue or bone marrow precursor cells, treating fertility  
 CC disorders, etc.

XX Sequence 352 AA;

Query Match 100.0%; Score 1849; DB 17; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 3.1e-171;  
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTSSLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60  
 DB 1 MTSSLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60  
 QY 61 PTLNRPVSRALRTALOHILGVPOGALLDNRDECELIISFAETGLSTINOTRDLRHFSS 120  
 DB 61 PTLNRPVSRALRTALOHILGVPOGALLDNRDECELIISFAETGLSTINOTRDLRHFSS 120  
 QY 121 DRTAGREVOQASLMFVQPSNTTWTLKRVLYLVGPHNTLTATQYLLLEVDAASGMHOL 180  
 DB 121 DRTAGREVOQASLMFVQPSNTTWTLKRVLYLVGPHNTLTATQYLLLEVDAASGMHOL 180  
 QY 121 DRTAGREVOQASLMFVQPSNTTWTLKRVLYLVGPHNTLTATQYLLLEVDAASGMHOL 180  
 DB 121 DRTAGREVOQASLMFVQPSNTTWTLKRVLYLVGPHNTLTATQYLLLEVDAASGMHOL 180  
 QY 181 PLGPEAQAACSGCHLTLELVLEGOVAOSSVILGGAHRRPVAARVGVGKHQIHRGIDC 240  
 DB 181 PLGPEAQAACSGCHLTLELVLEGOVAOSSVILGGAHRRPVAARVGVGKHQIHRGIDC 240  
 QY 241 OGGSRMCCROEFVDFRIGMDHMTIOPEGYAMNFCIGCCPLHAGMPGIAASFRHVALN 300  
 DB 241 OGGSRMCCROEFVDFRIGMDHMTIOPEGYAMNFCIGCCPLHAGMPGIAASFRHVALN 300  
 QY 301 LKANTAACTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVEACGCS 352  
 DB 301 LKANTAACTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVEACGCS 352

RESULT 2  
 AAB70530  
 ID AAB70530 standard; protein: 352 AA.

XX AAB70530:  
 DT 08-MAY-2001 (first entry)

DE Human TGF-beta MP121 protein sequence SEQ ID NO:4.  
 XX  
 KW Human: transforming growth factor-beta; monomeric protein; MP52;  
 KW MP121: dimeric protein; TGF-beta; vulnerable; antidiabetic; nootropic;  
 KW neuroprotective; antifertility; osteopathic; gene therapy; bone;  
 KW cartilage; dental; wound healing; connective tissue.

OS Homo sapiens.

XX Key Location/Qualifiers  
 FT Misc-difference 316 /note="unspecified"

XX EP1074620-A1.

XX 07-FEB-2001.  
 XX  
 XX 06-AUG-1999; 99EP-0115613.  
 PF  
 XX  
 XX 06-AUG-1999; 99EP-0115613.  
 PR  
 XX  
 XX (HYGE-) HYGENE AG C/O MAEDER & BAUMGARTNER TREUH.  
 PA WPI: 2001-228100/24.  
 DR N-PSDB: AAF74421.

PT Novel monomeric protein of transforming growth factor-beta family for  
 PT prevention or therapy of diseases associated with bone, cartilage  
 PT damage, promotion of wound healing, has substitution or deletion of  
 PT cysteine

PS Claim 10; page 21-22; 31pp; English.

XX The present invention describes a protein (I) selected from the members  
 CC of the transforming growth factor-beta (TGF-beta) superfamily, which is  
 CC monomeric due to substitution or deletion of a cysteine which is  
 CC responsible for dimer formation. Also described are: (1) nucleic acid  
 CC (II) encoding (1): (2) expression vector (III) containing (II) in a  
 CC suitable vector system; (3) host cell (IV) containing (III) capable of  
 CC producing (I); and (4) a pharmaceutical composition (V) containing (I),  
 CC (II), (III) or (IV). (1) has vulnerability, antileuk, nootropic,  
 CC neuroprotective, antifertility and osteopathic activities, and can be  
 CC used in gene therapy. (V) is useful for the prevention or therapy of  
 CC diseases for which also the dimeric form of the protein would be  
 CC indicated. Diseases treatable include diseases associated with bone  
 CC and/or cartilage damage or affecting bone and/or cartilage disease or  
 CC situations in which cartilage and/or bone growth is desirable, for spinal  
 CC including tendon and/or ligament, periodontal and dental tissue including  
 CC dental implants, neural tissue including CNS tissue and neuropathological  
 CC situations, tissue of the sensory system, liver, pancreas, cardiac,  
 CC blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane,  
 CC endothelium, epithelium, for promotion or induction of nerve growth,  
 CC tissue regeneration, angiogenesis, wound healing including ulcers, burns,  
 CC injuries or skin grafts, induction of proliferation of progenitor cells  
 CC or bone marrow cells, for maintenance of a state of proliferation or  
 CC differentiation, for treatment or preservation of tissue or cells for  
 CC organ or tissue transplantation, for integrity of gastrointestinal lining  
 CC and for treatment of disturbances in fertility, contraception or  
 CC pregnancy. The present sequence represents the specifically claimed  
 CC TGF-beta monomeric protein MP121, from the present invention.

XX Sequence 352 AA;

Query Match 99.4%; Score 1838; DB 22; Length 352;  
 Best Local Similarity 99.7%; Pred. No. 3.6e-170;  
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTSSLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60  
 DB 1 MTSSLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSILDKLHLTOR 60  
 QY 61 PTLNRPVSRALRTALOHILGVPOGALLDNRDECELIISFAETGLSTINOTRDLRHFSS 120  
 DB 61 PTLNRPVSRALRTALOHILGVPOGALLDNRDECELIISFAETGLSTINOTRDLRHFSS 120  
 QY 121 DRTAGREVOQASLMFVQPSNTTWTLKRVLYLVGPHNTLTATQYLLLEVDAASGMHOL 180  
 DB 121 DRTAGREVOQASLMFVQPSNTTWTLKRVLYLVGPHNTLTATQYLLLEVDAASGMHOL 180  
 QY 181 PLGPEAQAACSGCHLTLELVLEGOVAOSSVILGGAHRRPVAARVGVGKHQIHRGIDC 240  
 DB 181 PLGPEAQAACSGCHLTLELVLEGOVAOSSVILGGAHRRPVAARVGVGKHQIHRGIDC 240  
 QY 241 OGGSRMCCROEFVDFRIGMDHMTIOPEGYAMNFCIGCCPLHAGMPGIAASFRHVALN 300  
 DB 241 OGGSRMCCROEFVDFRIGMDHMTIOPEGYAMNFCIGCCPLHAGMPGIAASFRHVALN 300



QY 301 LKNTAGTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGCS 352  
 |||  
 Db 301 LKNTAGTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGCS 352

## RESULT 3

AAM60617  
 ID AAM60617 standard; Protein: 352 AA.

AC AAM60617:

DT 01-FEB-1999 (first entry)

DE Murine liver activin beta c polypeptide.

KW Liver activin; beta c; beta e; cell differentiation; hematopoiesis;  
 erythroid; ovarian follicular maturation; hormone; neuronal survival;

KW spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;  
 osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;

KW menstrual disorder; transgenic; modulator.

OS Mus sp.

FT Key Location/Qualifiers

FT Peptide 1..20

FT Modified-site /note="signal sequence"

FT Modified-site /note="Asn is putatively N-glycosylated"

FT Modified-site /note="Asn is putatively N-glycosylated"

FT Modified-site /note="Asn is putatively N-glycosylated"

FT Modified-site /note="Asn is putatively N-glycosylated"

FT Domain /note="propeptide domain"

FT Cleavage-site /note="endoproteolytic cleavage site"

FT Domain /note="mature growth factor domain"

PN MO9822492-A1.

PD 28-MAY-1998.

XX 20-NOV-1997: 97MO-US20882.

XX 20-NOV-1996: 96US-0752919.

XX (UNMI ) UNIV MICHIGAN.

PI Bonadio J, Fang J;

XX WPI: 1998-312408/27.

DR N-PSDB: AAV38237.

XX New isolated nucleic acid encoding sub-units of liver activin -

PT useful for regulating growth and differentiation of cells, e.g. for

PT treating liver, bone and hematopoietic disorders

XX Claim 16: Fig 1: 14pp: English.

XX This represents a murine liver activin beta c polypeptide. Sequences

CC derived from beta c cDNA clone is used for screening and cloning a liver

CC activin beta c gene. Disorders of cell growth or differentiation (or

CC susceptibility to them) are diagnosed by measuring liver activin gene

CC activity or by detecting a mutation in the liver activin gene. Disorders

CC of hematopoiesis, erythroid differentiation, ovarian follicular

CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone

CC formation, insulin secretion or cardiac morphogenesis are some conditions

CC that can be diagnosed using the liver activin. Cell growth and

CC differentiation can be stimulated by treatment with an liver activin

CC compound or agent that upregulates the compound's expression. Antagonists  
 CC can be used to treat liver diseases while agonists can be used to  
 CC increase growth and regeneration of liver tissue. The liver activin  
 CC compound may also induce bone growth (e.g. for treating osteoporosis or  
 CC osteomalacia) or hematopoiesis, particularly erythropoiesis, e.g. for  
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies  
 CC are useful in immunoassays, to generate anti-idiotypic antibodies (which  
 CC bind to liver activin receptors) and to inhibit liver activin. Also,  
 CC transgenic animals containing liver activin gene can be used to produce  
 CC the liver activin (in correctly processed and modified forms) proteins,  
 CC or the transgenic animals, are useful for screening for liver activin  
 CC modulators.

SQ Sequence 352 AA:

Query Match 75.3%; Score 1392; DB 19; Length 352;

Best Local Similarity 75.9%; Pred. No. 8.5e-127; Mismatches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;

QY 1 MTSSLLAFLLAPPTVATPRAGGCPACGCPRLHESQRELLDLAKSLDKLHLTOR 60

Db 1 MASSLLALLFLPTTVVNPVKTEGPCACWGALFDESORELLDLAKSLDKLHLTOR 60

QY 61 PTLNRPVSAURLTALOHLDGVPQALAE-DNREOCETISFAETGLSTINOTRLDFHFS 119

Db 61 PTLNRPVSAURLTALOHLDGVPQALAE-DNREOCETISFAETGLSTINOTRLDFHFS 120

QY 120 SRTAGDREVGQASLMFVQPLPSNTTWTLKRVLYLGPHTNTLATQYLEVDASGMQ 179

Db 121 G-RMAGMEVROTREFVQFPNATQNMIRVLYLKPDTNLTLSQYVQVAVASGMQ 179

QY 180 LPLGPEAQAACSGHLTLLEVGVAOSSVITLGAARHPVAVARVVGKRRKRGID 239

Db 180 LPLGPEAQAACSGHLTLLEVGVAOSSVITLGAARHPVAVARVVGKRRKRGID 239

QY 240 COGSMCCROEFVDFREIHWIIOPEGYAMNFCIGOCPLIAGMPSIAPFHTAVL 299

Db 240 COGSMCCROEFVDFREIHWIIOPEGYAMNFCIGOCPLIAGMPSIAPFHTAVL 299

QY 300 NLKNTAGTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGCS 352

Db 300 NLKNTAGTGGSCCVPTARRPLSLYYDRDSNVKTDIPDMVVEACGCS 352

## RESULT 4

AAR92754  
 ID AAR92754 standard; Protein: 350 AA.

AC AAR92754:

DT 21-JUL-1996 (first entry)

DE Human growth differentiation factor-12.

XX Growth differentiation factor-12; GDF-12; liver; cell proliferation;

XX cancer; diagnosis; therapy; transforming growth factor beta.

XX Homo sapiens.

FT Key Location/Qualifiers

FT Modified-site /label="N-glycosylation\_site"

FT Cleavage-site /label="C-terminal\_region"

FT Region /label="GFR-12 active C-terminal fragment"

PN MO9602559-A1.

PD 01-FEB-1996.

XX 12-JUL-1995: 95WO-US08745.

PR 26-SEP-1994; 94US-0311370.  
 PR 13-JUL-1994; 94US-0274215.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.  
 XX  
 PT Esqueja AF, Lee S;  
 XX  
 DR WPI: 1996-105850/11.  
 DR N-PSDB: AAT16883.  
 XX  
 PT DNA encoding Growth Differentiation Factor-12 - used in diagnostic  
 PT and therapeutic methods esp. in methods for treating a cell  
 PT proliferative disorder of liver origin  
 XX  
 PS Claim 3; Page 40-43; 52pp; English.  
 XX  
 CC Human growth differentiation factor-12 (GDF-12 - AAR92754) is a new  
 CC member of the transforming growth factor beta superfamily that is  
 CC expressed specifically in liver. It can be obt'd. by expression  
 CC of a cDNA clone (AAT16883) derived from adult liver in transformed  
 CC host cells. GDF-12 possesses activities that will make it useful  
 CC in the treatment of liver disorders, e.g. disease states in which  
 CC liver function is compromised, or cellular proliferative disorders  
 CC such as hepatocellular carcinoma. In can also be used to expand  
 CC liver cells in culture and to raise diagnostic antibodies.  
 XX  
 SO Sequence 350 AA:  
 Query Match 35.9%; Score 664; DB 17; Length 350;  
 Best Local Similarity 43.3%; Pred. No. 5,1e-56;  
 Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;  
 YY 9 FLLAPTTVATPRAGGCGCPACGCTLELESORELLDLAKRSITDKLHTQRPILNRPVS 68  
 DB 9 WLVLMLALVBAQGTGVCPCGCGSKLAPQAEALVLELAKQOILDGHLTSRPRITHP 68  
 YY RALATLALHGVPOGALLDNRDECEIISFAE-TGLSTINOTRLDHFSSDRTAGDR 127  
 DB 69 QALTLRALRLQ---PGSVAPNGE---EVISFATVTDSTSAVSSLTFTLSTPRS---H 119  
 YY 128 EVOQASLMFVQLPSNTWTMLKRVIVLGP---HNTNLTLATQYLLEVDASGWHOLPLG 183  
 DB 120 HLYHARLMLHV-LPT-LPGTLCLRTFRMGPRRRRROGSRITLAEHHTNL---GWHTLTLP 174  
 YY 184 PEAQACSGHLLTEL---VLEGO---VAQSSVILGGAH-RPFVAVRVYG--GKHQIH 234  
 DB 175 SSGLRGKSGVYLKQLDCLRPLEGNSTVTGQPRRLDPTAGHQOPLFLKIRANEPGAGRAR 234  
 YY 235 RRGIDCGGSRMCCROEFVDFREIGMHWMILOPEGYAMNFCIGCCPLIAGMPGIAASF 294  
 DB 235 RRTPTCEPATPLCCRRDHVDFQELGMRDWIILQPEGYQYNVCSGCGCPHLAGSPGIAASF 294  
 YY 295 HTAVLNLKANT--AGTTGGGSCCVPTARRPLSLIYDROSNIVKTDIPDMVVEACGS 352  
 DB 295 HSAVFSLLKANNPWPAST---SCCVPTARRPLSLIYDROSNIVKTDIPDMVVEACGS 350  
 RESULT 5  
 AAM93672  
 ID AAM93672 standard; Protein; 350 AA.  
 XX  
 AC AAM93672;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 3558.  
 XX  
 KM Human; full length cDNA; cDNA synthesis; oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX

PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114089.  
 XX  
 PR 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 DR WPI: 2001-524255/58.  
 DR N-PSDB: AAK94607.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 3558; 1380pp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5'- and 3'-ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesized by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC encoded by a full length human cDNA of the invention.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 XX  
 SO Sequence 350 AA:  
 Query Match 35.9%; Score 664; DB 22; Length 350;  
 Best Local Similarity 43.3%; Pred. No. 5,1e-56;  
 Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;  
 YY 9 FLLAPTTVATPRAGGCGCPACGCTLELESORELLDLAKRSITDKLHTQRPILNRPVS 68  
 DB 9 WLVLMLALVBAQGTGVCPCGCGSKLAPQAEALVLELAKQOILDGHLTSRPRITHP 68  
 YY RALATLALHGVPOGALLDNRDECEIISFAE-TGLSTINOTRLDHFSSDRTAGDR 127  
 DB 69 QALTLRALRLQ---PGSVAPNGE---EVISFATVTDSTSAVSSLTFTLSTPRS---H 119  
 YY 128 EVOQASLMFVQLPSNTWTMLKRVIVLGP---HNTNLTLATQYLLEVDASGWHOLPLG 183  
 DB 120 HLYHARLMLHV-LPT-LPGTLCLRTFRMGPRRRRROGSRITLAEHHTNL---GWHTLTLP 174  
 YY 184 PEAQACSGHLLTEL---VLEGO---VAQSSVILGGAH-RPFVAVRVYG--GKHQIH 234  
 DB 175 SSGLRGKSGVYLKQLDCLRPLEGNSTVTGQPRRLDPTAGHQOPLFLKIRANEPGAGRAR 234  
 YY 235 RRGIDCGGSRMCCROEFVDFREIGMHWMILOPEGYAMNFCIGCCPLIAGMPGIAASF 294  
 DB 235 RRTPTCEPATPLCCRRDHVDFQELGMRDWIILQPEGYQYNVCSGCGCPHLAGSPGIAASF 294  
 YY 295 HTAVLNLKANT--AGTTGGGSCCVPTARRPLSLIYDROSNIVKTDIPDMVVEACGS 352  
 DB 295 HSAVFSLLKANNPWPAST---SCCVPTARRPLSLIYDROSNIVKTDIPDMVVEACGS 350  
 RESULT 6  
 AAM60619  
 ID AAM60619 standard; Protein; 350 AA.  
 XX  
 AC AAM60619;  
 XX  
 DT 01-FEB-1999 (first entry)  
 XX

XX	Human liver activin beta e polypeptide.
KX	Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
KW	erythroid; ovarian follicular maturation; hormone; neuronal survival;
KM	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
KW	osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoassay;
KM	menstrual disorder; transgenic; modulator; human.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Peptide
FT	Location/Qualifiers
FT	1..17
FT	/note="signal sequence"
FT	18..236
FT	/note="propeptide domain"
FT	198..200
FT	/note="asn is putatively N-glycosylated"
FT	232..236
FT	/note-"endoproteolytic cleavage site"
FT	237..350
FT	/note-"mature growth factor domain"
PV	
PN	WO9822492-A1.
XX	
XX	28-MAY-1998.
PD	
XX	
XX	20-NOV-1997; 97MO-US20882.
PR	
XX	20-NOV-1996; 96US-0752919.
PA	(UNMI) UNIV MICHIGAN.
PI	
DR	Bonadio J, Fang J:
XX	
XX	MP1: 1998-312408/27.
PT	N-PSTDB: AAV38240.
PT	New isolated nucleic acid encoding sub-units of liver activin - useful for regulating growth and differentiation of cells, e.g. for treating liver, bone and hematopoietic disorders
PS	
XX	Disclosure; Fig 5; 14pp; English.
CC	This represents a human liver activin beta e polypeptide. The invention provides murine beta c and beta e polypeptides and the encoding genes. Disorders of cell growth or differentiation (or susceptibility to them) are diagnosed by measuring liver activin gene activity or by detecting a mutation in the liver activin gene. Disorders of haematopoiesis, erythroid differentiation, ovarian follicular maturation, hormone secretion, neuronal survival, spermatogenesis, bone formation, insulin secretion or cardiac morphogenesis are some conditions that can be diagnosed using the liver activin. Cell growth and differentiation can be stimulated by treatment with an liver activin compound or agent that upregulates the compound's expression. Antagonists can be used to treat liver diseases while agonists can be used to increase growth and regeneration of liver tissue. The liver activin compound may also induce bone growth (e.g. for treating osteoporosis or osteomalacia) or haematopoiesis, particularly erythropoiesis, for treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies are useful in immunoassays, to generate anti-idiotypic antibodies (which bind to liver activin receptors) and to inhibit liver activin. Also, transgenic animals containing liver activin gene can be used to produce the liver activin (in correctly processed and modified forms) proteins, or the transgenic animals, are useful for screening for liver activin modulators.
SQ	Sequence 350 AA:
Query Match	35.4%; Score 655; DB 19; Length 350;
Best Local Similarity	42.8%; Pred. No. 3,9e-55;
Matches 154; Conservative	54; Mismatches 118; Indels 34; Gaps 14
9 FLALLPTVATPRAGGCPACGGPTLELSQRELLDLAKRSIDKHLTGPRTNPVS 68	

Db	9	WLVLLMALVLR	AGTGSVCPSCGSKLAPQERALVLELAKQILLLEGHLNLSRPRTITPP	68
Oy	69	RAALRTALQHLHGVPQ	GALLLEDNREQECETISFAE-TGLSTINQTRLDFHPSDRTAGDR	127
Db	69	QAAYTRALRLRQ---	PGSAVPGNCE---EVISEFATVTDSTSAVSSLLTFHILSTPRS---	119
Oy	128	EYQASLSLFEFVQLP	STNTWTLYKRVLYLGP-----HNINLTLAYQYLEVDSAGMHQPLG	183
Db	120	HLYHARLWLVH-VLP	TLPQTLCLIRFERMGRRRRROGSRKTLAEHNITNL---GWHTTLPL	174
Oy	134	PEAQAACSGCHLTLEL	---VLEGQ---VAQSSVILGAAH-RPVAARVRVG--GKHQIH	234
Db	175	SSGLRGEKSGYLTQLQ	DCRPLLEGNSTVTGPPRRLLDPAGHQOPLLEKIRANEGCAGRAR	234
Oy	235	RRGIDCGGSRMCCROE	FFDFREIGWHDNITQPEGYAMNFCIGQCPHLIAGMPGIAASF	294
Db	235	RRTPPTCEPRTPLCC	RDRHYVDFOELSKRMIILQPGVQLNCSQCPRHLAGGPEIAASF	294
Oy	295	HTVALNLLKAMT---	AAATGGGSCQVPFARRPRLSLYYDRDSNIVKTDIPDMVAVGCGS	352
Db	295	HSVAFSLKANNMWPAST	----SCCVPTARRPCLSLLYLDHNGMNVKTDVPMVAEACGCS	350
RESULT 7				
AAM60618				
ID	AAM60618 standard; protein; 350 AA.			
XX				
AC	AAM60618;			
XX				
DT	01-FEB-1999 (first entry)			
XX				
DE	Murine liver activin beta e polypeptide.			
XX				
KW	Liver activin; beta c; beta e; cell differentiation; hematopoiesis;			
KW	erythroid; ovarian follicular maturation; hormone; neuronal survival;			
KW	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;			
KW	osteomacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay;			
XX	menstrual disorder; transgenic; modulator.			
OS	Mus sp.			
XX				
FH	Key			
FT	Peptide			
FT	Location/Qualifiers			
FT	1..21			
FT	/note="signal sequence"			
FT	Domain			
FT	22..236			
FT	/note="propeptide domain"			
FT	Modified-site			
FT	198..200			
FT	/note="asn is putatively N-glycosylated"			
FT	Cleavage-site			
FT	232..236			
FT	/note="endoproteolytic cleavage site"			
FT	Domain			
FT	237..349			
FT	/note="mature growth domain"			
XX				
XX	MO9822492-A1.			
XX				
PD	28-MAY-1998.			
XX				
XX	20-NOV-1997; 97WO-US20882.			
XX				
XX	20-NOV-1996; 96US-0752919.			
XX				
PA	(UNMT ) UNIV MICHIGAN.			
XX				
PI	Bonadio J, Fang J;			
XX				
DR	WPI: 1998-312408/27.			
XX				
DR	N-PSDB: AAV38238.			
XX				
PT	New isolated nucleic acid encoding sub-units of liver activin -			
PT	useful for regulating growth and differentiation of cells, e.g. for			
PT	treating liver, bone and hematopoietic disorders			
XX				
PS	Claim 16: Fig 2: 141pp; English.			

XX This represents a murine liver activin beta e polypeptide. Sequences  
CC derived from a beta c cdna clone is used for screening and cloning the  
CC activin beta e gene. Disorders of cell growth or differentiation (or  
CC susceptibility to them) are diagnosed by measuring liver activin gene  
CC activity or by detecting a mutation in the liver activin gene. Disorders  
CC of haematopoiesis, erythroid differentiation, ovarian follicular  
CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone  
CC formation, insulin secretion or cardiac morphogenesis are some conditions  
CC that can be diagnosed using the liver activin. Cell growth and  
CC differentiation can be stimulated by treatment with an liver activin  
CC compound or agent that upregulates the compound's expression. Antagonists  
CC can be used to treat liver diseases while agonists can be used to  
CC increase growth and regeneration of liver tissue. The liver activin  
CC compound may also induce bone growth (e.g. for treating osteoporosis or  
CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for  
CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies  
CC are useful in immunoassays, to generate anti-idiotypic antibodies (which  
CC bind to liver activin receptors) and to inhibit liver activin. Also,  
CC transgenic animals containing liver activin gene can be used to produce  
CC the liver activin (in correctly processed and modified forms) proteins,  
CC or the transgenic animals, are useful for screening for liver activin  
CC modulators.

Sequence 350 AA;

Query Match	35.08;	Score 648;	DB 19;	Length 350;
Best Local Similarity	42.48;	Pred. NO. 1.8e-54;		
Matches 153;	Conservative 58;	Mismatches 118;	Indels 32;	Gaps 14

[illegible]

RESULT 8	
AA92017	
ID	AA92017 standard; Protein; 407 AA.
IV	

AC	AAV92017,	
XX		
DT	19-JUL-2000 (first entry)	
XX		
DE	Human inhibin B beta subunit.	
XX		
KW	human inhibin B beta subunit; CKGF; mutant; cysteine knot growth factor.	
KW	hairpin loop; infertility.	
XX		
XS	Homo sapiens.	

XX	Key	Location/Qualifiers
PH	Misc-difference	1..307
FT	/note=	"optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
FT		
FT		
FT	Domain	308..328
FT	/label=	beta_hairpin_loop_1
FT	/note=	"mutant optionally comprises one or more substitutions in these residues"
FT		
FT	Misc-difference	329..375
FT	/note=	"optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
FT		
FT	Domain	376..400
FT	/label=	beta_hairpin_loop_3
FT	/note=	"mutant optionally comprises one or more substitutions in these residues"
FT		
FT	Misc-difference	401..407
FT	/note=	"optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"
FT		
XX		

PN WO200017360-A1  
XX

PD 30-MAR-2000

PF 19-MAR-1999; 99WO-US05908.  
VY

PR 22-SEP-1998; 98WO-US19772.  
YY

PA (UYMA-) UNIV MARYLAND BALTIMORE,  
XX

PI Weintraub BD, Szkudlinski MW;

WPI; 2000-283585/24

PT New mutant cysteine knot growth factor proteins comprising one or more  
PT mutant subunits, useful for treating or preventing diseases e.g.  
PT hypothyroidism and thyroid cancer  
xx

PS Claim 298; page 304; 320pp; English  
xy

CC This is the wild type human inhibin B beta subunit  
CC Mutants compared at least

CC beta halophilin loop, resulting in increased bioactivity.

mutant subunits and having novel properties or improved pharmacological properties compared to wild type subunits.

superfamily comprises at least four families of growth factors: the

the neurotrophins and the transforming growth factor- $\beta$  family; the families are known to be structurally similar (approximately 20% sequence identity).

positions in the CKGF hairpin loops of family members and other members

Sequence 407 AA;

Query Match	32.4%	Score 559.5	DB 21	Length 407
Best Local Similarity	36.6%	Pred. No. 1.2e-49		
Matches 145; Conservative	60	Mismatches 118	Indels 73	Gaps 16

```

QY 13 APTTVANPRA-----GGQ---CPACGGPTLETSOREL-----LIDLAKRSILD 53
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 29 SPTTPPPAAPPPPPPPGSGSDOTCTSCGG---FRPELGNVDGDFLEAVKRIHS 84
      :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 54 KLHLTORPTLNRPYSKALRTALDHLGVCPOGALLDNR-----EQQC 96
      :| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : |||

```

```

Db 85 RLOMGRPNITHAVPKAAWVTAALRLHA---GKVRDGRVEIPLHLDGHAAPGADGGERVS 141
QY 97 EIIISFAETGLSTINOTRLDFHSSDRTAGDRE--VOQASLMFVQLPSTWTTL----- 148
Db 142 EIIISFAETDGLASSRVLRYFISNE---GNQLFVQASLMVLYLKL---LPVLEKGSRR 195
QY 149 KVRVLVL---GPHNTNLTAQYLLLEVDAAGWHLPLGPEAQAACSGHLLTLELVYEGV 205
Db 196 KVRKVVYFOEGHGRDWMN-VEKRVDLKRSQWHTFPLTEALFEGERRLNDVQCD 254
QY 206 AGSSVIL-----GGAHRPEVAARVVG-GKHQIHRGIDCGSGRMCCROEFVDFRE 258
Db 255 CQELAVVPVFDPEESHRPVPVQARLDGSRHRIKRGLEDGRTNLCCROOFFIDFRL 314
QY 259 IGMHDMITIOPEGYAMNFCIGCCPLHIAAGPGIAASFHTAVLNLKANTAGTTGG--GSC 316
Db 315 IGMHDMITAPGYGNYCGSGCPALAGPGSASSHTAVVNOYRMR---GLNPGTVNSC 371
QY 317 CVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
Db 372 CIPTKLSTMSMLYFDDEYNIVKRDVPMIVVECGCA 407

RESULT 9
AAV92019 standard; Protein: 407 AA.
ID AAV92019
AC AAV92019:
XX 19-JUL-2000 (first entry)
XX Human activin B subunit.
DE human activin B subunit; CKGF; mutant; cystine knot growth factor;
KW hairpin loop; fertility.
XX Homo sapiens.
OS
XX
FT Key Location/Qualifiers
FT Misc-difference 1..307 /note= "optionally mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
FT Domain 308..328
FT /label= beta_hairpin_loop_1
FT /note= "mutant optionally comprises one or more
FT substitutions in these residues"
FT Misc-difference 329..375 /note= "optionally mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
FT Domain 376..400
FT /label= beta_hairpin_loop_3
FT /note= "mutant optionally comprises one or more
FT substitutions in these residues"
FT Misc-difference 401..407 /note= "optionally mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
XX
XX WO200017360-A1.
XX
XX 30-MAR-2000.
XX
XX 19-MAR-1999: 99WO-US05908.
XX
XX 22-SEP-1998: 98WO-US19772.
XX
XX (UYMA-) UNITV MARYLAND BALTIMORE.
XX
XX Weintraub BD, Szudlinski MJ;
XX
XX MPI: 2000-283585/24.

```

```

XX
PT New mutant cystine knot growth factor proteins comprising one or more
PT mutant subunits, useful for treating or preventing diseases e.g.
PT hypothyroidism and thyroid cancer
XX
PS Claim 328: Page 305; 320pp; English.
XX
CC This is the wild type human activin B subunit.
CC Mutants comprise at least one electrostatic charge altering mutation in a
CC beta hairpin loop, resulting in increased bioactivity.
CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more
CC mutant subunits and having novel properties or improved pharmacological
CC properties, compared to wild type CKGFs, are claimed. The CKGF
CC superfamily comprises at least four families of growth factors: the
CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
CC the neurotrophins and the transforming growth factor-beta family; the
CC families are known to be structurally similar (especially comprising the
CC cystine knot topology) and it was shown that mutations at certain
CC positions in the CKGF hairpin loops of family members and other members
CC of the CKGF superfamily could significantly alter the biological
CC activities of the CKGF.
CC Mutant transforming growth factor family proteins or analogues are useful
CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained
CC infertility, time-limited conception and in assisted reproduction.
XX
SQ Sequence 407 AA:
32.4%; Score 599.5; DB 21; Length 407;
Query Match Best Local Similarity 36.6%; Pred. No. 1.2e-49;
Matches 145; Conservative 60; Mismatches 118; Indels 73; Gaps 16;
QY 13 APTVATPRA-----GGQ---CPAGSGPTLELESOREL-----LIDLAKRSILD 53
Db 29 SPTPEPTAAAPPPPPGSGSDPTCTSCGG---FRPEELGRVDGFLVAVKRHILS 84
QY 54 KLHLTORPLNRPVSRALRTALQHLHGVPQCALLEDNR-----EOEC 96
Db 85 RLOMGRPNITHAVPKAAWVTAALRLHA---GKVRDGRVEIPLHLDGHAAPGADGGERVS 141
QY 97 EIIISFAETGLSTINOTRLDFHSSDRTAGDRE--VOQASLMFVQLPSTWTTL----- 148
Db 142 EIIISFAETDGLASSRVLRYFISNE---GNQLFVQASLMVLYLKL---LPVLEKGSRR 195
QY 149 KVRVLVL---GPHNTNLTAQYLLLEVDAAGWHLPLGPEAQAACSGHLLTLELVYEGV 205
Db 196 KVRKVVYFOEGHGRDWMN-VEKRVDLKRSQWHTFPLTEALFEGERRLNDVQCD 254
QY 206 AGSSVIL-----GGAHRPEVAARVVG-GKHQIHRGIDCGSGRMCCROEFVDFRE 258
Db 255 CQELAVVPVFDPEESHRPVPVQARLDGSRHRIKRGLEDGRTNLCCROOFFIDFRL 314
QY 259 IGMHDMITIOPEGYAMNFCIGCCPLHIAAGPGIAASFHTAVLNLKANTAGTTGG--GSC 316
Db 315 IGMHDMITAPGYGNYCGSGCPALAGPGSASSHTAVVNOYRMR---GLNPGTVNSC 371
QY 317 CVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
Db 372 CIPTKLSTMSMLYFDDEYNIVKRDVPMIVVECGCA 407

RESULT 10
AAP70204
ID AAP70204 standard; protein: 353 AA.
XX
XX AAP70204:
XX
XX 09-APR-1991 (first entry)
XX
XX Sequence of human inhibin beta-chain precursor beta-B.
XX
XX Fertility control; contraception; hormone; spermatogenesis.
XX
XX Homo sapiens.
XX
XX

```

```

XX Key Location/Qualifiers
FH Modified-site 38..40
FT /note="potential N-linked glycosylation sites"
FT Region 1..237
FT /note="used to design a long synthetic DNA probe"
FT Protein 238..343
FT Cleavage-site 235..237
FT /note="proteolytic processing site"
XX EP222491-A.
XX 20-MAY-1987.
XX 02-OCT-1986; 86EP-0307586.
XX 12-SEP-1986; 86US-0906729.
XX 03-OCT-1985; 85US-0783910.
XX 10-FEB-1986; 86US-0827710.
XX (GETH ) GENENTECH INC.
XX Mason AJ, Seeburg PH;
XX WPI: 1987-137512/20.
XX N-PSDB: AAN70316.
XX Recombinant human or porcine inhibin or activin - used for
XX modulating clinical condition or reproductive physiology of
XX animals.
XX Disclosure: Fig 9A; 48pp; English.
XX
XX A compsn. comprising human or porcine inhibin which is completely
XX free of unidentified or porcine proteins is claimed. Also claimed
XX are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
XX chain. Sequencing of inhibin-encoding cDNA has led to the
XX identification of prodomain regions located N-terminal to the
XX mature inhibin chains that represent coordinately expressed
XX biologically active polypeptides. The prodomain regions or
XX prodomain immunogens are useful in monitoring preproinhibin
XX processing in transformant cell culture or in experiments directed
XX at modulating the clinical cond. or reproductive physiology of
XX animals.
XX
XX Sequence 353 AA:
XX
Query Match 31.9%; Score 590; DB 8; Length 353;
Best Local Similarity 37.3%; Pred. No. 8,1e-49;
Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;
XX
QY 26 CPACGGPTLELSOREL-----LDDIAKRSILDKLHTORPTLNRPSRAALPTALOHL 79
DB 1 CTSCGG----FRPEELGRVDGDFLEAVKRIHSRLMRGPNTHAVPKAMVTALRL 56
QY 80 HGVPGALLDNR-----EQECETISFAETGISTINQTRIDLFHSSDR 122
DB 57 HA---GKVEDDREVEIPHLDGHASPGADQGEVSEISFAETDGLASSRVLYFTSNB- 112
QY 123 TAGDRE--VQOASLMRFVQLPSNTMTL-----KAVVLY--GPHNTNLTATQYLE 171
DB 113 --GNNLFFVQASLMVLYKL--LPVYLEKSGRRKRVKVFQDQGHDRNMN-VEKHYD 166
QY 172 VDSAGMHLPLGPEAOACSGHLLTLELVLEGVQAOSSVL-----CGAARPPVAVARV 225
DB 167 LKRSQMHFPLLEATIALFERGERRLNLVQCCSCQELAVVPVFDPEESHREPVVQA 226
QY 226 RVG-GKHQIHRRGIDQGGSRMCROEFVDFREIGHMDITIOEGYAMNFCIGCPH 284
DB 227 RLDSNRHRIKRGLECDGRTNLCRQGFIDFLIGMDIILAPTYGNCCESSCPAYL 286
QY 285 AGMGCIASFHTAVNLKANTAGTGC--GSCCVTAHRPUSLLYYDRDSNTVKTDIP 342

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DB 287 AGVPGSASSPHAVNOYMR---GLNPGTVNSCCIPTKLSTMSMLYFDEYNIYKRDVP 343
QY 343 DMVFEACGS 352
DB 344 NMIVECGCA 353
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RESULT 11
ID AAF70201
ID AAF70201 standard; protein; 351 AA.
XX
AC AAF70201;
XX
DT 09-APR-1991 (first entry)
XX
DE Sequence of porcine inhibin beta-chain precursor beta-B.
XX
KM Fertility control; contraception; hormone; spermatogenesis.
XX
OS Sus scrofa domestica.
XX
XX Key Location/Qualifiers
FH Region 1..270
FT /note="used to design a long synthetic DNA probe"
FT Protein 271..386
FT Cleavage-site 268..270
FT /note="proteolytic processing site"
XX
XX EP222491-A.
XX 20-MAY-1987.
XX 02-OCT-1986; 86EP-0307586.
XX 12-SEP-1986; 86US-0906729.
XX 03-OCT-1985; 85US-0783910.
XX 10-FEB-1986; 86US-0827710.
XX (GETH ) GENENTECH INC.
XX Mason AJ, Seeburg PH;
XX WPI: 1987-137512/20.
XX N-PSDB: AAN70316.
XX Recombinant human or porcine inhibin or activin - used for
XX modulating clinical condition or reproductive physiology of
XX animals.
XX Disclosure: Fig 2B; 48pp; English.
XX
XX A compsn. comprising human or porcine inhibin which is completely
XX free of unidentified or porcine proteins is claimed. Also claimed
XX are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
XX chain. Sequencing of inhibin-encoding cDNA has led to the
XX identification of prodomain regions located N-terminal to the
XX mature inhibin chains that represent coordinately expressed
XX biologically active polypeptides. The prodomain regions or
XX prodomain immunogens are useful in monitoring preproinhibin
XX processing in transformant cell culture or in experiments directed
XX at modulating the clinical cond. or reproductive physiology of
XX animals.
XX
XX Sequence 351 AA:
XX
Query Match 31.3%; Score 578; DB 8; Length 351;
Best Local Similarity 37.3%; Pred. No. 1.2e-47;
Matches 128; Conservative 62; Mismatches 111; Indels 42; Gaps 9;
QY 44 LDLAKRSILDKLHTORPTLNRPSRAALRTALQHLHGVPGCALLEDNR----- 92
DB 17 LEAVKRIHRLRQGRPNITHAVPKAMVTALRLHA---GKVEDGVEIPLHDGHS 73

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XX 12-SEP-1985; 86US-0906729.  
 PR 03-OCT-1985; 85US-0783910.  
 PR 10-FEB-1986; 86US-0827710.  
 XX (GETH ) GENENTECH INC.  
 XX PI Mason AJ, Seeburg PH;  
 XX DR WPI; 1987-137512/20.  
 XX N-PSDB; AAN70315.  
 XX PT Recombinant human or porcine inhibin or activin - used for  
 XX PT modulating clinical condition or reproductive physiology of  
 XX PT animals.  
 XX PS Disclosure; Fig 8a; 48pp; English.  
 XX CC A compsn. comprising human or porcine inhibin which is completely  
 CC free of unidentified or porcine proteins is claimed. Also claimed  
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta  
 CC chain. Sequencing of inhibin-encoding cDNA has led to the  
 CC identification of prodomain regions located N-terminal to the  
 CC mature inhibin chains that represent coordinately expressed  
 CC biologically active polypeptides. The prodomain regions or  
 CC prodomain immunogens are useful in monitoring preproinhibin  
 CC processing in transformant cell culture or in experiments directed  
 CC at modulating the clinical cond. or reproductive physiology of  
 CC animals.  
 XX CC  
 SQ Sequence 426 AA;  
 Query Match 30.1%; Score 557; DB 8; Length 426;  
 Best Local Similarity 31.5%; Pred. No. 1.7e-45;  
 Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12;

OY 6 LLAFLLAFTTATPRAG-----QCPACGGPTL--ELSEORELLDLAKRSJDKLHLT 58  
 DB 10 LLAFCITVRSSEPTSECHSAAPDCSCALALPKDVPNSOPEVEAVKHIIMLHKK 69  
 OY 59 QRPILNRPVSRALRPLALH-----GVPQALLDNRDECELSFAET 104  
 DB 70 KRPDVTQPPKALLNAIKLHKGKGVETIEDDIGRAENELMEOTSEITTAES 129  
 OY 105 GLSTLNQRLDHFSSDRPAGRE-VQASLMFVQLP-SNTTWT-LKVRVLVLP--- 158  
 DB 130 GVA-----RKLHFEISKESDLSVERAEVWLFLKVPKNNRRTKTYTLFOQKHPG 184  
 OY 159 -----NTNLTATVYLEVDASGWHQLPLCPKPAACSGHLELVLEG 203  
 DB 185 SLDTGEAEVGLKGERSELILSEKVVDAKRSWHPVSSSTIOPLDQKSSLDVRIAC 244  
 OY 204 QVAOSS-----VILG-----GA-----AHRPF--VAARVRVCK 230  
 DB 245 EOCQSGSASLVILGKKKKKEEGEGKKKGGEGGAGADEKEOSHHPFLMLQROSEDP 304  
 OY 231 HOIHRGIDCQSGSMWCRQEFVDFREIGMDWIIQPGYAMNFCIGCPLIAGMPGI 290  
 DB 305 HRRRRRGLECDGKVNICKKQFFVSKFDIGMDWIIAPSGYAHNVEGEGPSIIAGTSGS 364  
 OY 291 AASPTAVLNLLKATTAAGTGGSCCVPTARRPUSLTYRDSNIYKTDIPDMVYACG 350  
 DB 365 SLSPHSTVINHYRMGRHSPANLKCSCVFTKLRLPMISMLTYDDGONITIKDIOMIYEECG 424  
 OY 351 CS 352  
 DB 425 CS 426

RESULT 14  
 ID AAY92016  
 XX AAY92016 standard; Protein: 426 AA.

AC AAY92016;  
 XX 19-JUL-2000 (first entry)  
 DT XX  
 DE Human inhibin A beta subunit.  
 XX human inhibin A beta subunit; CKGF; mutant; cystine knot growth factor;  
 KW hairpin loop; infertility.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Misc-difference 1..325 /note= "optionally mutated to increase electrostatic  
 FT interaction between beta hairpin structure and  
 FT a receptor"  
 FT Domain 326..346 /label= beta\_hairpin\_loop-1  
 FT /note= "mutant optionally comprises one or more  
 FT substitutions in these residues"  
 FT Misc-difference 347..394 /note= "optionally mutated to increase electrostatic  
 FT interaction between beta hairpin structure and  
 FT a receptor"  
 FT Domain 395..419 /label= beta\_hairpin\_loop-3  
 FT /note= "mutant optionally comprises one or more  
 FT substitutions in these residues"  
 FT Misc-difference 420..426 /note= "optionally mutated to increase electrostatic  
 FT interaction between beta hairpin structure and  
 FT a receptor"  
 FT FT  
 FT WO200017360-A1.  
 PD 30-MAR-2000.  
 PD 19-MAR-1999; 99WO-US05908.  
 PR 22-SEP-1998; 98WO-US19772.  
 PA (UYMA-) UNIV MARYLAND BALTIMORE.  
 PA Weintrub BD, Szekulinski MW;  
 PI WPI; 2000-283585/24.  
 DR New mutant cystine knot growth factor proteins comprising one or more  
 XX mutant subunits, useful for treating or preventing diseases e.g.  
 XX hypothyroidism and thyroid cancer  
 PT Claim 283; Page 303; 320pp; English.  
 PS This is the wild type human inhibin A beta subunit.  
 XX Mutants comprise at least one electrostatic charge altering mutation in a  
 CC beta hairpin loop, resulting in increased bioactivity.  
 CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more  
 CC mutant subunits and having novel properties or improved pharmacological  
 CC properties, compared to wild type CKGFs, are claimed. The CKGF  
 CC superfamily comprises at least four families of growth factors: the  
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,  
 CC the neurotrophins and the transforming growth factor-beta family; the  
 CC cystine knot topology and it was shown that mutations at certain  
 CC positions in the CKGF hairpin loops of family members and other members  
 CC of the CKGF superfamily could significantly alter the biological  
 CC activities of the CKGF.  
 CC Mutant transforming growth factor family proteins or analogues are useful  
 CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained  
 CC infertility, time-limited conception and in assisted reproduction.  
 XX Sequence 426 AA;

Query Match	30.1%	Score 557	DB 21	Length 426
Best Local Similarity	31.5%	Pred. No. 1.7e-45		
Matches 133	Conservative 74	Mismatches 135	Indels 80	Gaps 12
OY	6	LLAFLLAPTTVAAPRAG-----QPCAGCGPTL--ELESQRELLDLAKRSITLKLHLT	58	
DB	10	LLASCMITIVRSSPTGSGCHSAAPDCPSALALPKVDVNSQPEVNAVKHILNKLHLK	69	
OY	59	ORPLTNRPVSRAALRTALQHLH-----GVPGALLLEDNRQECETISFAET	104	
DB	70	KRPDTQVPRKALNALIKRLHVKGVGNGYVEIEDIGIRAEEMNLMDQTSITITFAES	129	
OY	105	GLSTINGTRLDHFSSDRTAGDRE--VQOASLMEFYQLP-SNTTW-LKRVLYLGFH---	158	
DB	130	GFA-----RKTLEHFEISKSGDLSYVERAEVMLFLTKVPKRNRTKVTIRLFGQOKHPQG	184	
OY	159	-----NTNITLATQYILLEVDASGMHQLPRLGPEQAQSCGHLTLELVES	203	
DB	165	SLDTGEAEVEYGLKGRSEELLSEKVVADARKSTWHFPPVSSLTQRLDDGKSSLDVRIAC	244	
OY	204	QVAQSS-----VLG-----GA-----AHRPF--VAARVRVGK	230	
DB	245	BQCGEGASGLVLLGKKKKKEEGEGKKKCGECGACADEKEQSHRPFMLQAROSEDPH	304	
OY	231	HQIHRRGIDCGGSRMCCHQEFVDFREIGMHDMTIQEGYANFCIGCCPLHIAGMPGI	290	
DB	305	HRRRRGLDGDGVNICKKKOFFVSRKIDGMNMTIAPSGYHANYCEGEGPSHIAGTSGS	364	
OY	291	AASFHAYVNLKLKANTAGCTGGSCCVPTRRRPLSLLYVDRDSNIYKTDIPMYVEACG	350	
DB	365	SLSFHSTVINHYMRHSPFANLKSQCVPTKLKPMSLYLLDDQNLTKDIONNIIVECG	424	
OY	351	CS 352		
DB	425	CS 426		
RESULT 15				
AA92018				
ID	AA92018	standard; Protein; 426 AA.		
XX	AA92018:			
AC				
XX	19-JUL-2000	(first entry)		
DT				
XX				
DE		Human activin A subunit.		
KX		human activin A subunit; CKGF; mutant; cysteine knot growth factor;		
KW		hairpin loop; infertility.		
XX				
OS		Homo sapiens.		
XX				
Key		Location/Qualifiers		
FT	MISC-difference 1..325	/note="optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"		
FT				
FT	Domain	326..346		
FT		/label="beta_hairpin_loop_1"		
FT		/note="mutant optionally comprises one or more substitutions in these residues"		
FT	MISC-difference 347..394	/note="optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"		
FT				
FT	Domain	395..419		
FT		/label="beta_hairpin_loop_3"		
FT		/note="mutant optionally comprises one or more substitutions in these residues"		
FT	MISC-difference 420..426	/note="optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"		
FT				

XX MN WO200017360-A1.

XX PD 30-MAR-2000.

XX PF 19-MAR-1999; 99WO-US05908.

XX PR 22-SEP-1998; 98WO-US19772.

PA (UYMA-) UNIV MARYLAND BALTIMORE.

PI Weintraub BD, Szkudlinski MW;

XX DR WPI: 2000-283585/24.

XX PT New mutant cystine knot growth factor proteins comprising one or more

XX PT mutant subunits, useful for treating or preventing diseases e.g.

XX PT hypothyroidism and thyroid cancer

PS Claim 313; Page 304; 320pp; English.

XX

XX This is the wild type human activin A subunit.

XX CC Mutants comprise at least one electrostatic charge altering mutation in a

XX CC beta hairpin loop, resulting in increased bioactivity.

XX CC Mutant cystine knot growth factor (CKGF) proteins comprising one or more

XX CC mutant subunits and having novel properties or improved pharmacological

XX CC properties, compared to wild type CKGFs, are claimed. The CKGF

XX CC superfamily comprises at least four families of growth factors: the

XX CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,

XX CC the neurotrophins and the transforming growth factor-beta family; the

XX CC families are known to be structurally similar (especially comprising the

XX CC cystine knot topology) and it was shown that mutations at certain

XX CC positions in the CKGF hairpin loops of family members and other members

XX CC of the CKGF superfamily could significantly alter the biological

XX CC activities of the CKGF.

XX CC Mutant transforming growth factor family proteins or analogues are useful

XX CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained

XX CC infertility, time-limited conception and in assisted reproduction.

XX

XX Sequence 426 AA:

XX

XX

XX Query Match 30.1%; Score 557; DB 21; Length 426;

XX Best Local Similarity 31.5%; Pred. No. 1,7e-45;

XX Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12

QY 6 LLAFLIAPTVAAPRAG-----QCPACGGPTL--ELESORELLDLAKSITDKLNT 58

DB 10 LLASGMIVRSPTPGSEGHSAAPDCSCALALPKVDVPSQPMVEAVKKNHILMLNLK 69

QY 59 QRPITNRPVSKAALRALDNLH-----GVPGALLDNEDECEISFAET 104

DB 70 KRPDVTPAPKALLNAIKRLHGVKGCENGVEIEDDIGRAEMNELMEQTSITTFAPS 129

QY 105 GLSTINQRPDLDFHSSDDPRAGDRE-VQOASIMFEVQLP-SNTWT-LKVRVLYLAPR--- 158

DB 130 GVA-----RKLTHFETSKESGSDLSVERAEVYLFELKPKARKARTKRYVIRLFGQOKNPRG 184

QY 159 -----NTNLTLATQYLLEVDAAGNHOPLRGFAOAGCSOGILTLELVLEG 203

DB 185 SLDTGEAEAEVGLKGERSELLSEKXVDARKSTHNVFVSSIQRLDLQKGSLSLDVRIAC 244

QY 204 QVAQSS---VILG-----GA-----AHRPF--VAARVAVGK 230

DB 245 ECGQESGASLVILGKKKKKKEEGGKKGKGEGGAGADEEKBOGSHRPFMLDAROSEDPH 304

QY 231 HOIHRRGIDCGGSRKCCROEPFYDFEIGHNMTIOPEGYAMNFCIGCPRIHAGMPGI 290

DB 305 HRRRRRGLECDGKVNICCKKFOFVSKDIGNNDMIASGYHANYCEGECPSHITAGTSGS 364

QY 291 AASFHRAVNLKLANTAAGTGGGSCCVPTARRPLSLIYYDSDNIVKQIDPDVAVACG 350

DB 365 SLSTFHSHTVNHVYRMGRGSHPPANLKSVCVPTKLKRPMSMLTYDDGONLIKDKIDNMIVCEG 424

Tue Oct 15 13:49:39 2002

us-09-684-383-2.rag

Page 12

QY 351 CS 352  
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Db 425 CS 426

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Job time : 43 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 12, 2002, 02:05:12 ; Search time 15.5 Seconds  
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554.697 Million cell updates/sec

Title: US-09-684-383-2  
Perfect score: 1849  
Sequence: 1 MTSSLIAFLAFLAPTVATP.....DSNIVKTDIPDMVVEACGCS 352

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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4: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/BACKFILEST.pep:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1849	100.0	352	1	US-08-482-577B-2
2	1849	100.0	352	3	US-08-289-222E-4
3	1849	100.0	352	4	US-09-218-176-2
4	1849	100.0	352	4	US-09-054-526B-4
5	1398	75.6	352	1	US-08-482-577B-4
6	1398	75.6	352	4	US-09-218-176-4
7	664	35.9	350	5	PCT-US95-08745-14
8	664	35.9	350	5	PCT-US95-08745-14
9	590	31.9	106	1	US-08-459-214-31
10	590	31.9	106	3	US-08-289-222E-28
11	590	31.9	106	4	US-09-218-176-7
12	590	31.9	106	4	US-09-054-526B-28
13	590	31.9	353	1	US-08-197-792-43
14	590	31.9	353	1	US-08-459-850-43
15	590	31.9	353	1	US-08-459-214-43
16	587	31.7	349	1	US-08-197-792-33
17	587	31.7	349	1	US-08-459-850-33
18	587	31.7	349	1	US-08-459-214-33
19	587	31.7	349	1	US-08-197-792-31
20	562	30.4	424	1	US-08-459-850-31
21	562	30.4	424	1	US-08-459-214-31
22	557	30.1	426	1	US-08-197-792-41
23	557	30.1	426	1	US-08-459-850-41
24	557	30.1	426	1	US-08-459-214-41
25	457	24.7	127	1	US-08-455-550-11
26	440	23.8	119	2	US-08-274-215A-12
27	440	23.8	119	2	US-08-765-662-12

28	440	23.8	119	4	US-09-184-933-12	Sequence 12, Appl
29	440	23.8	119	5	PCT-US95-08745-12	Sequence 12, Appl
30	391	21.1	128	4	US-08-455-550-12	Sequence 12, Appl
31	389	21.0	147	4	US-08-065-844A-7	Sequence 7, Appl
32	388.5	21.0	121	1	US-08-581-529B-18	Sequence 18, Appl
33	388.5	21.0	121	1	US-08-455-559-24	Sequence 24, Appl
34	388.5	21.0	121	2	US-08-525-596B-28	Sequence 28, Appl
35	388.5	21.0	121	2	US-08-581-528A-18	Sequence 18, Appl
36	388.5	21.0	121	3	US-09-097-616-18	Sequence 18, Appl
37	388.5	21.0	121	3	US-09-177-860A-28	Sequence 28, Appl
38	388.5	21.0	121	4	US-09-145-060-24	Sequence 24, Appl
39	388.5	21.0	121	5	PCT-US94-00657-24	Sequence 24, Appl
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41	388.5	21.0	121	5	PCT-US94-07799-18	Sequence 18, Appl
42	380.5	20.6	120	1	US-08-481-377-22	Sequence 22, Appl
43	380.5	20.6	120	2	US-08-491-835-20	Sequence 20, Appl
44	380.5	20.6	120	3	US-09-153-733A-22	Sequence 22, Appl
45	380.5	20.6	120	3	US-08-946-092A-20	Sequence 20, Appl

# ALIGNMENTS

RESULT 1  
US-08-482-577B-2  
Sequence 2, Application US/08482577B  
Patent No. 5807713  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTHOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARNELESTEIN, MURRAY, AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
STREET: SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-577B-2  
Query Match 100.0%; Score 1849; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
1 MTSSLIAFLAFLAPTVATPAGCGPCTLELSORBLDLAKRSILDKLHLTOR 60

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Db 1 MTSSLLAFLLAPTTVATPRAGGCPACGGPTLEESRELLDLAKRSILDKLHTOR 60
QY 61 PTLNRPVSRAALRTALQHLHGVPOGALLLEDNREDECEITISFAETGLSTINOTRLDPHFSS 120
Db 61 PTLNRPVSRAALRTALQHLHGVPOGALLLEDNREDECEITISFAETGLSTINOTRLDPHFSS 120
QY 121 DRTAGDREVQOASLMFVQLPSNTTWLTKRVLYLGPNTNLTATQYLLLEDVDSAGMHOL 180
Db 121 DRTAGDREVQOASLMFVQLPSNTTWLTKRVLYLGPNTNLTATQYLLLEDVDSAGMHOL 180
QY 181 PLGPEAQAACSGHLLTELVEGVQAOSSVILGGAHRRFVAARVVGKHOIHRGIDC 240
Db 181 PLGPEAQAACSGHLLTELVEGVQAOSSVILGGAHRRFVAARVVGKHOIHRGIDC 240
QY 241 OGGSRMCCROEFVDFREIGWHDWIIQPEGYAMNFCIGQCPHLIAGMGIASFTAVLN 300
Db 241 OGGSRMCCROEFVDFREIGWHDWIIQPEGYAMNFCIGQCPHLIAGMGIASFTAVLN 300
QY 301 LKANTAGTGGSCCPTARPLSLIYDRDSNIYKTDIPDMVVEACGS 352
Db 301 LKANTAGTGGSCCPTARPLSLIYDRDSNIYKTDIPDMVVEACGS 352

```

## RESULT 2

```

US-08-289-222E-4
; Sequence 4, Application US/08299222E
; Patent No. 6120760
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, GERTRUD
; APPLICANT: NEIDHARDT, HELGE
; APPLICANT: BECHTOLD, ROLF
; APPLICANT: POHL, JENS
; TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM
; STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/289,222E
; FILING DATE: 25-AUG-1999
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,222
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE P 44 23 190.3
; FILING DATE: 07-JUL-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EPO 92102324.8
; FILING DATE: 12-FEB-1992
; APPLICATION NUMBER: PCT/EP93/00350
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: KITTIS, MONICA CHIN
; REGISTRATION NUMBER: 36,105
; REFERENCE/DOCKET NUMBER: P564-9021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202/638-5000
; TELEFAX: 202/638-4810
; INFORMATION FOR SEQ ID NO: 4:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 352 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-289-222E-4

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Query Match 100.0%; Score 1849; DB 3; Length 352;
Best Local Similarity 100.0%; Pred. No. 1,3e-180;
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MTSSLLAFLLAPTTVATPRAGGCPACGGPTLEESRELLDLAKRSILDKLHTOR 60
Db 1 MTSSLLAFLLAPTTVATPRAGGCPACGGPTLEESRELLDLAKRSILDKLHTOR 60
QY 61 PTLNRPVSRAALRTALQHLHGVPOGALLLEDNREDECEITISFAETGLSTINOTRLDPHFSS 120
Db 61 PTLNRPVSRAALRTALQHLHGVPOGALLLEDNREDECEITISFAETGLSTINOTRLDPHFSS 120
QY 121 DRTAGDREVQOASLMFVQLPSNTTWLTKRVLYLGPNTNLTATQYLLLEDVDSAGMHOL 180
Db 121 DRTAGDREVQOASLMFVQLPSNTTWLTKRVLYLGPNTNLTATQYLLLEDVDSAGMHOL 180
QY 181 PLGPEAQAACSGHLLTELVEGVQAOSSVILGGAHRRFVAARVVGKHOIHRGIDC 240
Db 181 PLGPEAQAACSGHLLTELVEGVQAOSSVILGGAHRRFVAARVVGKHOIHRGIDC 240
QY 241 OGGSRMCCROEFVDFREIGWHDWIIQPEGYAMNFCIGQCPHLIAGMGIASFTAVLN 300
Db 241 OGGSRMCCROEFVDFREIGWHDWIIQPEGYAMNFCIGQCPHLIAGMGIASFTAVLN 300
QY 301 LKANTAGTGGSCCPTARPLSLIYDRDSNIYKTDIPDMVVEACGS 352
Db 301 LKANTAGTGGSCCPTARPLSLIYDRDSNIYKTDIPDMVVEACGS 352

```

## RESULT 3

```

US-09-218-176-2
; Sequence 2, Application US/09218176
; Patent No. 6171584
; GENERAL INFORMATION:
; APPLICANT: HOTTEN, Gertrud
; APPLICANT: NEIDHARDT, Helge
; APPLICANT: BECHTOLD, Rolf
; APPLICANT: POHL, Jens
; APPLICANT: PAULISTA, Michael
; TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP
; STREET: 655 Fifteenth Street, N. W., G Street lobby,
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/218,176
; FILING DATE: Herewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/679,048
; FILING DATE: 12-JUL-1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP96/03065

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FILING DATE: 12-JUL-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP93/00350  
 FILING DATE: 2-FEB-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/482,577  
 FILING DATE: 7-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 92 102 324.8  
 FILING DATE: 12-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 44 23 190.3  
 FILING DATE: 01-JUL-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 195 11 243.1  
 FILING DATE: 27-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KITTS, MONICA CHIN  
 REGISTRATION NUMBER: 36,105  
 REFERENCE/DOCKET NUMBER: P564-6010  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202/638-5000  
 TELEFAX: 202/638-4810  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-218-176-2

Query Match 100.0%; Score 1849; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTSSLLAFLLAFTTVAATPRAGGCGPPTLEESORELLDLAKRSIIDKHLTOR 60  
 DB 1 MTSSLLAFLLAFTTVAATPRAGGCGPPTLEESORELLDLAKRSIIDKHLTOR 60  
 OY 61 PTLNRPVSRAALRTALQHLHGVPGALLDNRDQCEIISFAETGISTINOTRLDFHSS 120  
 DB 61 PTLNRPVSRAALRTALQHLHGVPGALLDNRDQCEIISFAETGISTINOTRLDFHSS 120  
 OY 121 DRTAGDREVOQASLMFVQLPSNTTWTLKVRVLVLPHTNNTLTAQYILLEVDASGMHOL 180  
 DB 121 DRTAGDREVOQASLMFVQLPSNTTWTLKVRVLVLPHTNNTLTAQYILLEVDASGMHOL 180  
 OY 181 PLGPEAOAASGCHLTLELVLEGVOAASSVILGGAARPFVAAARVVGKHOJHRRGIDC 240  
 DB 181 PLGPEAOAASGCHLTLELVLEGVOAASSVILGGAARPFVAAARVVGKHOJHRRGIDC 240  
 OY 241 QGSRMCCROEFFVDREIGMHWIIQPEGYAMNFCIGCCPLHIAIMPGLAASFHTAVLN 300  
 DB 241 QGSRMCCROEFFVDREIGMHWIIQPEGYAMNFCIGCCPLHIAIMPGLAASFHTAVLN 300  
 OY 301 LKANTAAGTTGGSCCVPTARRPLSLIYYDRDSNIVKTDIPMVEACGCS 352  
 DB 301 LKANTAAGTTGGSCCVPTARRPLSLIYYDRDSNIVKTDIPMVEACGCS 352

RESULT 4  
 US-09-054-526B-4  
 Sequence 4, Application US/09054526B  
 Patent No. 6197550  
 GENERAL INFORMATION:  
 APPLICANT: H. TITEN, GERT RUD  
 APPLICANT: NEIDHARDT, HELGE  
 APPLICANT: BECHTOLD, ROLF  
 APPLICANT: POHL, JENS  
 TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
 GROWTH/DIFFERENTIATION FACTORS  
 NUMBER OF SEQUENCES: 53

## CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAI DO, MARCEL STEIN, MURRAY & ORAM LLP  
 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
 STREET: SUITE 330  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005-5701  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patent In Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/054,526B  
 FILING DATE: 03-APR-1998  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/289,222  
 FILING DATE: 12-AUG-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 44 23 190.3  
 FILING DATE: 01-JUL-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EPO 92102324.8  
 FILING DATE: 12-FEB-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP93/00350  
 FILING DATE: 12-FEB-1993  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KITTS, MONICA CHIN  
 REGISTRATION NUMBER: 36,105  
 REFERENCE/DOCKET NUMBER: P564-8005  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202/638-5000  
 TELEFAX: 202/638-4810  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-054-526B-4

Query Match 100.0%; Score 1849; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-180;  
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTSSLLAFLLAFTTVAATPRAGGCGPPTLEESORELLDLAKRSIIDKHLTOR 60  
 DB 1 MTSSLLAFLLAFTTVAATPRAGGCGPPTLEESORELLDLAKRSIIDKHLTOR 60  
 OY 61 PTLNRPVSRAALRTALQHLHGVPGALLDNRDQCEIISFAETGISTINOTRLDFHSS 120  
 DB 61 PTLNRPVSRAALRTALQHLHGVPGALLDNRDQCEIISFAETGISTINOTRLDFHSS 120  
 OY 121 DRTAGDREVOQASLMFVQLPSNTTWTLKVRVLVLPHTNNTLTAQYILLEVDASGMHOL 180  
 DB 121 DRTAGDREVOQASLMFVQLPSNTTWTLKVRVLVLPHTNNTLTAQYILLEVDASGMHOL 180  
 OY 181 PLGPEAOAASGCHLTLELVLEGVOAASSVILGGAARPFVAAARVVGKHOJHRRGIDC 240  
 DB 181 PLGPEAOAASGCHLTLELVLEGVOAASSVILGGAARPFVAAARVVGKHOJHRRGIDC 240  
 OY 241 QGSRMCCROEFFVDREIGMHWIIQPEGYAMNFCIGCCPLHIAIMPGLAASFHTAVLN 300  
 DB 241 QGSRMCCROEFFVDREIGMHWIIQPEGYAMNFCIGCCPLHIAIMPGLAASFHTAVLN 300  
 OY 301 LKANTAAGTTGGSCCVPTARRPLSLIYYDRDSNIVKTDIPMVEACGCS 352  
 DB 301 LKANTAAGTTGGSCCVPTARRPLSLIYYDRDSNIVKTDIPMVEACGCS 352

RESULT 5  
US-08-482-577B-4  
Sequence 4, Application US/08482577B  
Patent No. 5807713  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-4810  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
US-08-482-577B-4

Query Match 75.6%; Score 1398; DB 1; Length 352;  
Best Local Similarity 76.2%; Pred. No. 1.4e-134;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MTSSLLAFLLAPTTVPATPRAGGCGPTLLESORELLDLAKRSTLDKHLTOR 60  
DB 1 MASSLLALLFTPTTVVAPKTEGPCPACGALFDESORELLDLAKRSTLDKHLTOR 60  
QY 61 PTLNPRVSAALRTALQHLGVQAGALL-DNREOCEISFAETGISTINOTRLDPFS 119  
DB 61 PILSRPVRGALKTALQRLRGRPRELLLEHDOOEYEITSPADTDSSTINOTRLDPFS 120  
QY 120 SDRTAGDREVOQASLAFYVQVQLDSNTTWLTKVRLVLAGPHTNLTATQYLEVDASGMQ 179  
DB 121 G-RMAASGMEVHQTREMFVQFPHNATQTMNIRVLRPYDTNLTLSQYVQVNASGMQ 179  
QY 180 LPLGPEQAASQGHLLLELVESQVAVSSVILGGAHRRFVAARVGVGKHQIHRGID 239  
DB 180 LLLGPEQAASQGHLLLELVESQVAVSSVILGGAHRRFVAARVGVGKHQIHRGID 239  
QY 240 CQGSRMCCROBEFVDFREIGHMDWIOPEGYAMNFCIGCPPLHAGMPGIAAFHRAVL 299  
DB 240 CQGSRMCCROBEFVDFREIGHMDWIOPEGYAMNFCIGCPPLHAGMPGIAAFHRAVL 299  
QY 300 NLKNTAAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIDPMVVEACGCS 352

DB 300 NLKNTAAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIDPMVVEACGCS 352

RESULT 6  
US-09-218-176-4  
Sequence 4, Application US/09218176  
Patent No. 6171584  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, Gertrud  
APPLICANT: NEIDHARDT, Helge  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, Jens  
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
FAMILY  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N.W., G Street Lobby,  
SUITE 330  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/218,176  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,048  
FILING DATE: 12-JUL-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03065  
FILING DATE: 12-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 2-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,577  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92 102 324,8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190,3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 11 243,1  
FILING DATE: 27-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: KITS, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-6010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-218-176-4

Query Match 75.6%; Score 1398; DB 4; Length 352;

Best Local Similarity 76.2%; Pred. No. 1,46-134;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

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OY 1 MTSLLAFLLAATVATPRAGGOCPCACGPPTLEESORELLDLARSLDKLHLTOR 60
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MASSLLALFLPTTVVNPTEGCPACGCAIFDLESORELLDLAKSLDKLHLTOR 60
OY 61 PTLNRPVRAALRTHLHGVPOGALLE-DNREOCEIISFAETGLSTINOTRLDPHRS 119
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 61 PLSRPVSRGALTKALQKRCPRRTLEHQROROEYEIISADLDSSINOTRLEFHS 120
OY 120 SDRFAGREVQOASLMEFVQLPSNTTWTLKVRVLYLGPHTNLTLATOLLEVDASGMHQ 179
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 121 C-RRASMGEVQTRPMFVQRPFNATQGMNIRVLYLRPYDTNLTLTQVYVQVNASGMWQ 179
OY 180 LPLPEAOACSGHLLLELVLEGVQAOSSVILGCAHRRPFVAARVVGKRIHRRGD 239
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 180 LLLPEAOACSGHLLLELVLEGVQAOSSVILGCAHRRPFVAARVVGKRIHRRGD 239
OY 240 CCGSRMCCROEFVDFREIGMHDIIQPEGYAMNFCIGCPLHAGPGIAASF 299
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 240 CCGSRMCCROEFVDFREIGMHDIIQPEGYAMNFCIGCPLHAGPGIAASF 299
OY 300 NLKANTAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 300 NLKANTAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352

```

RESULT 7  
US-08-765-662-14  
Sequence 14, Application US/08765662

Patent No. 5929213

GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,662

FILING DATE: 28-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal

ORIGINAL SOURCE:  
US-08-765-662-14

Query Match 35.9%; Score 664; DB 2; Length 350;  
Best Local Similarity 43.3%; Pred. No. 1,16-59;

Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

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OY 9 FLLAAPTVAATPRAGGOCPCACGPPTLEESORELLDLAKSLDKLHLTOR 68
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 9 WLVLMLALVRAQGTGVCPCSCGSKIAQAEALVLELAKODIILGHLTSRPRITHP 68
OY 69 RAALRTALQHLHGVPOGALLE-DNREOCEIISFAE-TGLSTINOTRLDPHRS 127
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 69 QAAITRALRLRQ---PSSVARGNE---EVSFATVSTSTSYSLTFHLSPPS---H 119
OY 128 EYQOASLMEFVQLPSNTTWTLKVRVLYLGP---HNTNLTLATOLLEVDASGMHQ 183
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 120 HLYARMLAHV-LPT-LPGTLCIRIFRNGRRRRRQSGRTLLAEHHTNL---GWHITLTP 174
OY 184 PEOAOACSGHLLLELVLEGVQAOSSVILGCAH-RPVAARVVG--GKHQIH 234
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 175 SSGLRGKSGVLLKQLDRCRPLEGNSVTGQPRRLDTAGHQPFLELKRANEPGAGRAR 234
OY 235 RRGIDCCGSRMCCROEFVDFREIGMHDIIQPEGYAMNFCIGCPLHAGPGIAASF 294
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 235 RRTPTCEPATPLCCRRDHYVDFQELGWRDMLIQPEGYOLNVCSCGCPPLHAGPGIAASF 294
OY 295 HTAVNLKANT--AGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGCS 352
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 295 HSAVFLKANNPMPAST---SCCVPTARRPLSLLYLDHNGVAVTDPDMVVEACGCS 350

```

RESULT 8  
PCT-US95-08745-14

Sequence 14, Application PC/TUS9508745

GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE

TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 350 amino acids  
TYPE: amino acids  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE: Internal

ORIGINAL SOURCE:  
PCT-US95-08745-14

Query Match 35.9%; Score 664; DB 5; Length 350;  
Best Local Similarity 43.3%; Pred. No. 1,1e-59;  
Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

OY 9 FLLAPPTVTPRAGCCPACGPTLLESOEELDLAKSTLIDKLHTOPPLNRPVS 68,  
DB 9 WLVLMLVRAOCTGSCPGSGSKLAPQARALVELAKQDILDLHTSPTTHPP 68  
OY 69 RAALRTALQHLHGVPCALLDNEQCEIISFAE-TGLSTINOTRLDPHFSSDPTAGDR 127  
DB 69 QAAITRALRLQ--PGSVAPNGE---EVSIFATVSTDSATYSLLFHLSTPS---H 119  
OY 128 EVOQASLMEFVQLPSNTWMLKAVLVLP---HNNLTALATOLLEVDASGMHQLPG 183  
DB 120 HLTHARLMLHV-LPT-LPGTLCRIFRMGPRRRRQSGRTLLAEHHTML---GMHTLTP 174  
OY 184 PEAQACSGHLLTEL---VLEGO---VAQSVTLGAAH-RPVVAARVRG--CKHGIH 234  
DB 175 SSGLRBKSGVLKQLDRCRLLEGSTYTGOPRRLDTRAGHOOPLELKRANERPGAGAR 234  
OY 235 RRGIDCGGSRMCCROEFFVDFRIGWHMIIQPEGYAMNFCIGCPPLHAGPQIASF 294  
DB 235 RRTPEEPATPLCCRRHDYVDFQELGRDMLQPEGYOLANCSGCCPHLAGPQIASF 294  
OY 295 HTAVLNLKANT--AGTTGGGSCVPTARRPLSLYYDRDSNIKTDIPDMVYACGCS 352  
DB 295 HSAVFSLKANNPMPAST---SCVPTARRPLSLYLDHNGVNVKTDVPMVYACGCS 350

RESULT 9  
US-08-482-577B-24

Sequence 24, Application US/08482577B  
Patent No. 5807713

GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
SUITE 330  
CITY: WASHINGTON  
STATE: DC

COUNTRY: USA  
ZIP: 20005

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B

FILING DATE:  
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON

REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-577B-24

Query Match 31.9%; Score 590; DB 1; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.3e-53;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 CCRQEFFVDFRIGWHMIIQPEGYAMNFCIGCPPLHAGPQIASPHTAVNLKANT 306  
DB 1 CCRQEFFVDFRIGWHMIIQPEGYAMNFCIGCPPLHAGPQIASPHTAVNLKANT 60  
OY 307 AGTTGGGSCVPTARRPLSLYYDRDSNIKTDIPDMVYACGCS 352  
DB 61 AGTTGGGSCVPTARRPLSLYYDRDSNIKTDIPDMVYACGCS 106

RESULT 10  
US-08-289-222E-28

Sequence 28, Application US/08289222E  
Patent No. 6120760

GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD

APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, JENS  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B

TITLE OF INVENTION: FAMILY  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
SUITE 330  
CITY: WASHINGTON  
STATE: DC

COUNTRY: USA  
ZIP: 20005-5701

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/289,222E

FILING DATE: 25-AUG-1999  
CLASSIFICATION: 424

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITS, MONICA CHIN

REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-9021

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear

MOLECULE TYPE: protein  
US-08-289-222E-28

Query Match 31.9%; Score 590; DB 3; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.3e-53;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 CCROEFFVDFREIGWHDWITIOPEGYAMNFCIOCPHIGMPCIAAFTAVNLKANT 306  
DB 1 CCROEFFVDFREIGWHDWITIOPEGYAMNFCIOCPHIGMPCIAAFTAVNLKANT 60

OY 307 AAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGS 352  
DB 61 AAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGS 106

## RESULT 11

US-09-218-176-7  
Sequence 7, Application US/09218176

Patent No. 6171584

GENERAL INFORMATION:

APPLICANT: H TREN, Gertrud

APPLICANT: BECHTOLD, Helge

APPLICANT: POHL, Jens

APPLICANT: PAULISTA, Michael

TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP

STREET: 655 Fifteenth Street, N. W., G Street Lobby,

STREET: Suite 330

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/218,176

FILING DATE: Herewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/679,048

FILING DATE: 12-JUL-1996

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP96/03065

FILING DATE: 12-JUL-1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 2-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/482,577

FILING DATE: 7-JUN-1995

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EP 92 102 324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE 195 11 243.1

FILING DATE: 27-MAR-1995

ATTORNEY/AGENT INFORMATION:

NAME: KITTS, Monica Chin

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-6010

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-218-176-7

Query Match 31.9%; Score 590; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 7.3e-53;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 247 CCROEFFVDFREIGWHDWITIOPEGYAMNFCIOCPHIGMPCIAAFTAVNLKANT 306  
DB 1 CCROEFFVDFREIGWHDWITIOPEGYAMNFCIOCPHIGMPCIAAFTAVNLKANT 60

OY 307 AAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGS 352  
DB 61 AAGTTGGSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGS 106

## RESULT 12

US-09-054-5268-28  
Sequence 28, Application US/090545268

Patent No. 6197550

GENERAL INFORMATION:

APPLICANT: H TREN, GERTRUD

APPLICANT: BECHTOLD, HELGE

APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL

GROWTH/DIFFERENTIATION FACTORS

NUMBER OF SEQUENCES: 53

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP

STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,

STREET: SUITE 330

CITY: WASHINGTON

STATE: DC

COUNTRY: USA

ZIP: 20005-5701

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/054,5268

FILING DATE: 03-APR-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 01-JUL-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITTS, MONICA CHIN

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-8005

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 28:

SEQUENCE CHARACTERISTICS:

LENGTH: 106 amino acids

TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-054-5268-28

Query Match 31.9%; Score 590; DB 4; Length 106;  
Best Local Similarity 100.0%; Pred. No. 73e-53;  
Matches 106; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 247 CCREFPVDFEIGMHWIIOPEGYAMNFCIGQCPHLAGMGIAAFHTAVLNLKANT 306  
DB 1 CCRREFPVDFEIGMHWIIOPEGYAMNFCIGQCPHLAGMGIAAFHTAVLNLKANT 60

QY 307 AAGTGGGSCCVPTARRPLSLYYDRDSNIVKTDIPDMVEACGS 352  
DB 61 AAGTGGGSCCVPTARRPLSLYYDRDSNIVKTDIPDMVEACGS 106

## RESULT 13

US-08-197-792-43  
Sequence 43, Application US/08197792  
Patent No. 5525488

GENERAL INFORMATION:  
APPLICANT: Anthony J. Mason  
APPLICANT: Peter H. Seeburg  
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08197, 792  
FILING DATE: 16-FEB-1994  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/958414  
FILING DATE: 08-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744207  
FILING DATE: 12-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/215456  
FILING DATE: 05-JUL-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/906729  
FILING DATE: 31-DEC-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/827710  
FILING DATE: 07-FEB-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/783910  
FILING DATE: 03-OCT-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 297P2D4  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 353 amino acids  
TYPE: amino acid

TOPOLOGY: linear  
US-08-197-792-43

Query Match 31.9%; Score 590; DB 1; Length 353;  
Best Local Similarity 37.3%; Pred. No. 4e-52;  
Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;

QY 26 CPACGPTLELESQREL-----LIDLAKRSILDKLHTORPTLNRPVSRALPTALQHL 79  
DB 1 CTSCGG-----FRPEELGRVGDLEAVKRIILSRLOHGRPNTHAVPKAMAYALARKL 56

QY 80 HGVPQALLDNR-----BOCEIISFAETGLSTIVQTRLDHFHSSDR 122  
DB 57 HA--GKVRREDGRVEIRPHLDGHASPGADQGRVSEIISFATDGLASSRVLYLFISME- 112

QY 123 TAGDRE--VQASLMFVQLPSNTTTL-----KRVLYV---GPHNTLTLATQYLE 171  
DB 113 --GNQNLFEVQASLMYLYKL---LPVYLEKSRKRVKVFQEQGHDRWMN-VERKVD 166

QY 172 VDSAGWHQLPLGPEAQACSGHLELVLEGOVQSSVLL-----GSAHRRPVYARV 225  
DB 167 LKRSQWHTFPPLTEALQALFERGERRLNDVQCSQELAVVPVVDGEESHRRPVVQA 226

QY 226 RVG-GKHQIHRRGIDCGGSRMCCROEFVDFREIGMHWIIOPEGYAMNFCIGQCPH 284  
DB 227 RLDSRHRIKRLGECGRTNLCCROQFFIDFRIGMNDMIATGYGNVCEGSPAYL 286

QY 285 AGMPGTAASPTAVLNLKANTAGTTGG--GSCVPTARRPLSLYYDRDSNIVKTDIP 342  
DB 287 AGVPGSASSFHTAVVQYRMR--GLNPCTVNSCIPKISTMSMLYFDEEYNIKRVDP 343

QY 343 DMVVEACGS 352  
DB 344 NMIVECGCA 353

## RESULT 14

US-08-459-850-43  
Sequence 43, Application US/08459850  
Patent No. 5665568

GENERAL INFORMATION:  
APPLICANT: Anthony J. Mason  
APPLICANT: Peter H. Seeburg  
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or  
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypept  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08459, 850  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/197792  
FILING DATE: 17-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/958414  
FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744207  
FILING DATE: 12-AUG-1991  
PRIOR APPLICATION DATA:

INFORMATION FOR SEQ ID NO: 43:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 353 amino acids  
TYPE: amino acid



APPLICATION NUMBER: 07/215466  
 FILING DATE: 05-JUL-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/906729  
 FILING DATE: 31-DEC-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/827710  
 FILING DATE: 07-FEB-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/783910  
 FILING DATE: 03-OCT-1985  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 297P205  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELETYPE: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 353 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-459-850-43

Query Match 31.9%; Score 590; DB 1; Length 353;  
 Best Local Similarity 37.3%; Pred. No. 4e-52;  
 Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;

26 CPACGGPTLEESOREL-----LIDLAKRSILDKLHLPRLNRPVSRALRALDHL 79  
 1 CTSCGG-----FRPEELGRVGDPLEAVKRLHLSRLQMRGRPNITHAVPKAMVATLAKL 56  
 80 HGVPGALLDNR-----EOECEISFAETGISTINOTRLDFHSSDR 122  
 57 HA--GKVEDGVEIPLHLDGASPGADGERSSEIISFAETDGLASSRVLYEFSINE- 112  
 123 TAGDRE--VOOASLMFVQVLPSTNTWTL-----KRVLVL--GPHNTNLTAQYLL 171  
 113 --GNQNLFFVQASLMVLYKL--LPVLEKSGSRKRVKVFQEGHDDRMN-VEKRYD 166  
 172 VDASGWHQLPLPEPAOACSGHLLLELVLEGVAQSSVIL-----GGAHRPPVAAV 225  
 167 LKRSQWHTFPLTEALQALFEGGERLNLVQDCSCQELAVVPVDPGEESHRRPFVVOA 226  
 226 RVG-GKHQIHRGIDCGGSMCCROEFVDFREIGHMDIIOPEGYAMNFCIGCCPLHI 284  
 227 RLDSRRIRIKRKGLCDGRTNLCROOFFIDRLIGMNDIILAPGYGNYCGSCPAVL 286  
 285 AGPGLIASFTAVLNLKANTAGTTCG--GSCCVPTARRPRLSLLYYDRDSNIVKTDIP 342  
 287 AGPGLIASFTAVLNLKANTAGTTCG--GSCCVPTARRPRLSLLYYDRDSNIVKTDIP 343  
 343 DMVVEACGS 352  
 344 NMIVECCGA 353

RESULT 15  
 US-08-459-214-43  
 Sequence 43, Application US/08459214  
 Patent No. 5716810  
 GENERAL INFORMATION:  
 APPLICANT: Anthony J. Mason  
 APPLICANT: Peter H. Seeburg  
 TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or  
 TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide  
 TITLE OF INVENTION: Using such Nucleic Acid  
 NUMBER OF SEQUENCES: 44  
 CORRESPONDENCE ADDRESS:  
 ADDRESS: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd

CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: palin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/459,214  
 FILING DATE: 02-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/197792  
 FILING DATE: 17-FEB-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/958414  
 FILING DATE: 08-OCT-1992  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/744207  
 FILING DATE: 12-AUG-1991  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/215466  
 FILING DATE: 05-JUL-1988  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/906729  
 FILING DATE: 31-DEC-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/827710  
 FILING DATE: 07-FEB-1986  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 06/783910  
 FILING DATE: 03-OCT-1985  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 297P206  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELETYPE: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 43:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 353 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-459-214-43

Query Match 31.9%; Score 590; DB 1; Length 353;  
 Best Local Similarity 37.3%; Pred. No. 4e-52;  
 Matches 138; Conservative 59; Mismatches 113; Indels 60; Gaps 14;

26 CPACGGPTLEESOREL-----LIDLAKRSILDKLHLPRLNRPVSRALRALDHL 79  
 1 CTSCGG-----FRPEELGRVGDPLEAVKRLHLSRLQMRGRPNITHAVPKAMVATLAKL 56  
 80 HGVPGALLDNR-----EOECEISFAETGISTINOTRLDFHSSDR 122  
 57 HA--GKVEDGVEIPLHLDGASPGADGERSSEIISFAETDGLASSRVLYEFSINE- 112  
 123 TAGDRE--VOOASLMFVQVLPSTNTWTL-----KRVLVL--GPHNTNLTAQYLL 171  
 113 --GNQNLFFVQASLMVLYKL--LPVLEKSGSRKRVKVFQEGHDDRMN-VEKRYD 166  
 172 VDASGWHQLPLPEPAOACSGHLLLELVLEGVAQSSVIL-----GGAHRPPVAAV 225  
 167 LKRSQWHTFPLTEALQALFEGGERLNLVQDCSCQELAVVPVDPGEESHRRPFVVOA 226  
 226 RVG-GKHQIHRGIDCGGSMCCROEFVDFREIGHMDIIOPEGYAMNFCIGCCPLHI 284  
 227 RLDSRRIRIKRKGLCDGRTNLCROOFFIDRLIGMNDIILAPGYGNYCGSCPAVL 286

Tue Oct 15 13:49:39 2002

us-09-684-383-2.rai

Page 10

OY	285	AGPBGAAASHPTAVINLLKANTACGTCG--GSCVPPAPRPLSLLYYDRSDNIIVKTDIP	342
		:           :           :	
Dd	287	ACPVGSSASPHTAIVNDYRMH---GLNPQTVNSCCIPKLSTMSMLFPDDEXNIVAKRDVP	343
OY	343	DMVEAECGS	352
		: : :   : :	
Dd	344	NMIVECGCA	353

Search completed: October 12, 2002, 02:10:48  
Job time : 17.5 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2002, 01:13:12 : Search time 27 Seconds  
(without alignments)  
1252.720 Million cell updates/sec

Title: US-09-684-383-2

Sequence: 1 MTSLLAFLLAPTTATP.....DSNIVKTDIPDMVAVCGCS 352

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: PIR71:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	1849	100.0	352	2	JC2466
2	1398	75.6	352	2	JC5366
3	1392	75.3	352	2	S70580
4	688.5	37.2	367	2	JC4151
5	648	35.0	350	2	JC5241
6	607.5	32.9	370	2	151199
7	605	32.7	408	2	S50899
8	599.5	32.4	407	1	A40150
9	595.5	32.2	411	2	B41398
10	587	31.7	349	1	WPGGB
11	573.5	31.0	393	2	150103
12	562	30.4	424	1	WPGGB
13	559	30.2	424	1	S31440
14	557	30.1	426	1	B24248
15	556.5	30.1	425	1	S50898
16	552.5	29.9	425	1	147072
17	552	29.9	424	1	B40905
18	547	29.6	413	2	JC4862
19	476	25.7	255	2	148235
20	353	19.1	115	2	PN0505
21	351	19.0	115	2	PN0506
22	325	17.6	115	2	PN0504
23	307.5	16.6	101	2	C36192
24	306.5	16.6	101	2	B36192
25	284.5	15.4	393	1	S37073
26	284	15.4	396	1	BMH02
27	282	15.3	102	2	A36192
28	281	15.2	394	2	S45355
29	277	15.0	373	2	PM0042

30	267	14.4	357	2	A39364	GDF-1 embryonic gr
31	261	14.1	398	2	JH0688	bone morphogenetic
32	253	13.7	372	2	C39364	GDF-1 embryonic gr
33	247	13.4	398	2	JH0687	bone morphogenetic
34	246.5	13.3	353	2	150607	bone morphogenetic
35	240	13.0	408	2	S58791	bone morphogenetic
36	239.5	13.0	313	2	151284	bone morphogenetic
37	237	12.8	402	2	A45056	osteogenic protein
38	237	12.8	510	2	A54798	Vg-1-related prote
39	236.5	12.8	405	2	150608	bone morphogenetic
40	235	12.7	513	1	BMH06	bone morphogenetic
41	231.5	12.5	408	1	BMH04	bone morphogenetic
42	231	12.5	365	2	T43286	cet-1 protein - Ca
43	231	12.5	408	2	S38343	bone morphogenetic
44	230.5	12.5	401	2	JH0689	bone morphogenetic
45	229.5	12.4	426	2	JH0690	bone morphogenetic

## ALIGNMENTS

## RESULT 1

inhibin beta-C chain precursor - human  
JC2466  
N:Alternate names: activin beta C chain  
C:Species: Homo sapiens (man)  
C:Date: 29-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 29-Oct-1999  
C:Accession: JC2466  
R:Hoellen, G.; Neidhardt, H.; Schneider, C.; Pohl, J.  
Biochem. Biophys. Res. Commun. 206, 608-613, 1995  
A:Title: Cloning of a new member of the TGF-beta family: A putative new activin betac  
A:Reference number: JC2466; M01D:95126961  
A:Accession: JC2466  
A:Molecule type: mRNA  
A:Residues: 1-352 <RHO>  
A:Cross-references: GB:X82540; NID:9669154; PIDN:CA57890.1; PID:9669155  
A:Experimental source: Liver  
C:Genetics:  
A:Gene: GDB:INHBC  
A:Cross-references: GDB:632884  
A:Map position: 2cen-2q13  
C:Superfamily: inhibin  
C:Keywords: glycoprotein  
F:1-16/Domain: signal sequence #status predicted <SIG>  
F:19-236/Domain: propeptide #status predicted <PRO>  
F:237-352/Product: activin beta C #status predicted <MAT>  
F:110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 100.0%; Score 1849; DB 2; Length 352;  
Best local similarity 100.0%; Pred. No. 6, 5e-159;  
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MTSLLAFLLAPTTATP	AGGCGGPTLEESORELLDIARSLDKLTLQR	60
DB	1	MTSLLAFLLAPTTATP	AGGCGGPTLEESORELLDIARSLDKLTLQR	60
OY	61	PTLRPVSRAALFTALQHLG	CVPGALLIEDNREDECEIISFAETGLSTINOTRLDFHSS	120
DB	61	PTLRPVSRAALFTALQHLG	CVPGALLIEDNREDECEIISFAETGLSTINOTRLDFHSS	120
OY	121	DRTAGDEVOQASLMFVQ	LPSTNTWLKVRVLVGPNTNLTATQVLLVDASGMHL	180
DB	121	DRTAGDEVOQASLMFVQ	LPSTNTWLKVRVLVGPNTNLTATQVLLVDASGMHL	180
OY	181	PLGEPAQACSGCHITL	ELVLEGQVQSSVILGGAHNPVAVRVGSKHDIRGIDC	240
DB	181	PLGEPAQACSGCHITL	ELVLEGQVQSSVILGGAHNPVAVRVGSKHDIRGIDC	240
OY	241	OGGRMCCROEFVDFE	RTIGMHWIIOPEGYAMNFCIGCPHIGMPGIAASFHTAVLN	300
DB	241	OGGRMCCROEFVDFE	RTIGMHWIIOPEGYAMNFCIGCPHIGMPGIAASFHTAVLN	300
OY	301	LLKANTAGTTGGGSC	VPFARPLSLIYYDRDSNIVKTDIPDMVAVCGCS	352

Db 301 LUKANTAGTGGSCCVPPTARRPLSLTYDRDSNIVKTDIPDMVVEACGCS 352

## RESULT 2

activin beta C - mouse  
JC5366  
C:Species: Mus musculus (house mouse)  
C>Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 26-Aug-1999  
C:Accession: JC5366  
R:Yang, J.; Wang, S.; Smiley, E.; Bonadio, J.  
Biochem. Biophys. Res. Commun. 231, 655-661, 1997  
A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhibit  
A:Reference number: JC5366; MUID:97224404  
A:Accession: JC5366  
A:Molecule type: DNA  
A:Residues: 1-352 <FAN>  
A:Cross-references: GB:U95962  
C:Comment: Activin beta C and beta E form a distinct subset of related activins.  
C:Genetics:  
A:Introns: 105/3  
C:Superfamily: Inhibin

Query Match 75.6% Score 1398; DB 2; Length 352;  
Best Local Similarity 76.2%; Pred. No. 3.1e-118;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

OY 1 MTSSLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSIDLKHLTOR 60  
Db 1 MASSLLALLFLPTTVVNPKEGPCACWGAIFLESORELLDLAKRSIDLKHLTOR 60  
OY 61 PTLNRPVSRALRTALQHLHVPQALIE-DNREDECEIISFAETGLSTINOTRLDFHS 119  
Db 61 PTLNRPVSRALRTALQHLHVPQALIE-DNREDECEIISFAETGLSTINOTRLDFHS 119  
OY 120 SDRPACREVOQASIMFVQLPSNTWTMLKRVVLGPHNTMLTATQYLLVDASGMHQ 179  
Db 121 G-RMAGSEVQRTFRMFVQEPFHNAOTMTNIRVLRYPYDNLTLTSQYVQVNASGMWQ 179  
OY 180 LPLGPEAOACSGHLLTELVEGOVASSVILGCAHPRVFAARVYRGKHQIHRGID 239  
Db 180 LPLGPEAOACSGHLLTELVEGOVASSVILGCAHPRVFAARVYRGKHQIHRGID 239  
OY 240 COGSRMCRQEFVDFVDRREIGMDMTIOPRGYAMNFCIGQCPHLIAGMPGIASTHTAVL 299  
Db 240 COGSRMCRQEFVDFVDRREIGMDMTIOPRGYAMNFCIGQCPHLIAGMPGIASTHTAVL 299  
OY 300 NLKANTAGTGGSCCVPPTARRPLSLTYDRDSNIVKTDIPDMVVEACGCS 352  
Db 300 NLKANTAGTGGSCCVPPTARRPLSLTYDRDSNIVKTDIPDMVVEACGCS 352

RESULT 3  
750580  
activin beta C precursor - mouse

C:Species: Mus musculus (house mouse)  
C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
C:Accession: S70580  
R:Lau, A.L.; Nishimoto, K.; Matzuk, M.M.  
Biochim. Biophys. Acta 1307, 145-148, 1996  
A:Title: Structural analysis of the mouse activin beta-C gene.  
A:Reference number: S70580; MUID:96283807  
A:Accession: S70580  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-352 <LAU>  
A:Cross-references: EMBL:U40772  
C:Genetics:  
A:Introns: 106/1  
C:Superfamily: Inhibin

Query Match 75.3% Score 1392; DB 2; Length 352;  
Best Local Similarity 75.9%; Pred. No. 1.1e-117;

Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;

OY 1 MTSSLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSIDLKHLTOR 60  
Db 1 MASSLLALLFLPTTVVNPKEGPCACWGAIFLESORELLDLAKRSIDLKHLTOR 60  
OY 61 PTLNRPVSRALRTALQHLHVPQALIE-DNREDECEIISFAETGLSTINOTRLDFHS 119  
Db 61 PTLNRPVSRALRTALQHLHVPQALIE-DNREDECEIISFAETGLSTINOTRLDFHS 119  
OY 120 SDRPACREVOQASIMFVQLPSNTWTMLKRVVLGPHNTMLTATQYLLVDASGMHQ 179  
Db 121 G-RMAGSEVQRTFRMFVQEPFHNAOTMTNIRVLRYPYDNLTLTSQYVQVNASGMWQ 179  
OY 180 LPLGPEAOACSGHLLTELVEGOVASSVILGCAHPRVFAARVYRGKHQIHRGID 239  
Db 180 LPLGPEAOACSGHLLTELVEGOVASSVILGCAHPRVFAARVYRGKHQIHRGID 239  
OY 240 COGSRMCRQEFVDFVDRREIGMDMTIOPRGYAMNFCIGQCPHLIAGMPGIASTHTAVL 299  
Db 240 COGSRMCRQEFVDFVDRREIGMDMTIOPRGYAMNFCIGQCPHLIAGMPGIASTHTAVL 299  
OY 300 NLKANTAGTGGSCCVPPTARRPLSLTYDRDSNIVKTDIPDMVVEACGCS 352  
Db 300 NLKANTAGTGGSCCVPPTARRPLSLTYDRDSNIVKTDIPDMVVEACGCS 352

## RESULT 4

activin beta D chain precursor - African clawed frog

C:Species: Xenopus laevis (African clawed frog)  
C>Date: 27-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
C:Accession: J04151  
R:Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.  
Biochem. Biophys. Res. Commun. 210, 581-588, 1995  
A:Title: Molecular cloning and functional analysis of a new activin beta subunit: a d  
A:Reference number: J04151; MUID:95275314  
A:Accession: J04151  
A:Molecule type: mRNA  
A:Residues: 1-367 <ODA>  
A:Cross-references: DDBJ:D49543; NID:9961512; PIDN:BA08494.1; PID:9961513  
A:Experimental source: embryo  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; mesoderm  
F:1-253/Domain: signal sequence #status predicted <SIG>  
F:254-367/Product: activin beta D chain #status predicted <MAT>  
F:64,155,161,208,230/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 37.2% Score 688.5; DB 2; Length 367;  
Best Local Similarity 40.4%; Pred. No. 3.3e-54;  
Matches 147; Conservative 65; Mismatches 125; Indels 27; Gaps 8;

OY 5 LLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSIDLKHLTORPTLN 64  
Db 15 LLLAFLLAPTTVATPRAGGCPACGPTLEESORELLDLAKRSIDLKHLTORPTLN 64  
OY 65 RVSRAALRTALQHLH-GVPGAL-----DNREDECEIISFAETGLSTINQ 111  
Db 67 HVPVGAVALANLRRLINKPRMEGLFGSNMSDNTENTDIDQSYELISAELEYTENS 126  
OY 112 TRLDHFSSDRPACREVOQASIMFVQLPSNTWTMLKRVVLGPHNTMLTATQYLL 171  
Db 127 ITLNFQTRDKQO-SAHVYQAHLMWLFKAKNTSQQNETIRLVLYQVAYSRRILISKE 185  
OY 172 VDASGMHQLPLGPEAOACSGHLLTELVEGOVASSVILGCAHPRVFAARVYRG 229  
Db 186 PRMTGMOFFSLKSMQLTFFDGNKSLQLELNCDDGCDVPLVLPNNNSHOPFLVAQAK 245  
OY 230 K-HQIHRGIDCOGSRMCRQEFVDFVDRREIGMDMTIOPRGYAMNFCIGQCPHLIAG 288  
Db 246 QSHHATKSLNCDONSNCRRDYVDFKIGMNMWIIKPEYQIYNGMGLCPMHTAGAP 305  
OY 289 GIASFHTAVNLKANTAGTGGSCCVPPTARRPLSLTYDRDSNIVKTDIPDMVVEA 348

Db 306 GMA5HTTTLNLIKANNI--QTAVNSCCVPTKRRPUSMLFDRNNVLTADIMAVEA 363  
 Oy 349 CGCS 352  
 Db 364 CGCS 367

## RESULT 5

JC5241

activin beta E chain precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 25-Apr-1997 #sequence\_revision 09-May-1997 #text\_change 29-Oct-1999

C:Accession: JC5241; JC5367

R:Yang, J.; Yin, W.; Smiley, E.; Wang, S.O.; Bonadio, J.

Biochem. Biophys. Res. Commun. 228, 669-674, 1996

A:Title: Molecular cloning of the mouse activin beta E subunit gene.

A:Reference number: JC5241; MUID:97096313

A:Contents: 11ver

A:Accession: JC5241

A:Molecule type: mRNA

A:Residues: 1-350 &lt;FRAN&gt;

A:Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522

R:Yang, J.; Wang, S.; Smiley, E.; Bonadio, J.

Biochem. Biophys. Res. Commun. 231, 655-661, 1997

A:Title: Gene coding for mouse activin beta C and beta E are closely linked and exhibit

A:Reference number: JC5366; MUID:97224404

A:Accession: JC5367

A:Molecule type: DNA

A:Residues: 1-350 &lt;FRAN&gt;

A:Cross-references: GB:U96386; NID:g2072521; PIDN:AAB53801.1; PID:g2072522

C:Genetics:

A:Insertions: 99/3

C:Superfamily: Inhibin

Query Match

Best Local Similarity 42.4%; Score 648; DB 2; Length 350;

Matches 153; Conservative 58; Mismatches 118; Indels 32; Gaps 14;

Oy 6 LLAFLAATTVAATPRAGGCGPPTLEESORELLDLAKRSILDKLHILTORPTLR 65  
 Db 8 LMLILMALVWVOSRRSA--CPSCGGPTLAPQGERALVLELAQOILEGHLHSRPRTIR 65  
 Oy 66 PVSRAALFTALQHLHGVQALLEDNRECELSIFA---ETGLSTINOTRLDFHFSRDR 122  
 Db 66 PLPQALATLRAIRLQ--PK-SWVPGNR--KVISFATITDKSTSY--KSMILFOLS--- 115  
 Oy 123 TAGDREVOOASLMFVQPLPSNTTTLKRVLVLGPHNTLTLATQYLLF--VDASGWHOL 180  
 Db 116 PLMSHILYHARL--WLVHVPSPFGTLYLHIFRCG--TTRCRGRTFLAEHQTSSGHNAL 171  
 Oy 181 PLGPEAQAACSGHILTELVLEGQVAOSS-----VILGAA--HREPVAAVRVYG--GKH 231  
 Db 172 TLPSGSLRSEDSGVVYLQLEFRPLDINSTAAGLPRLILLDAGQGRPLELKRANEPGAG 231  
 Oy 232 QIHRRGIDCGGSRMCCREFFVDREICGHMDITQREYAMNFCIGGCPHLHNGMPTIA 291  
 Db 232 RARRRTPCEPPTPLCCRDHYVDQELGWRMDILOPEYQOLNCSGCPHLHNGMPTIA 291  
 Oy 292 ASFHTAVLTLKANTAAAGTTGGSCCVPTARRPLSLLYRDSNIVATDIPDMVVEAGCG 351  
 Db 292 ASFHSVFLKANNP--WPAGSSCCVPTARRPLSLLYLDHNGVAVTDPDMVVEAGCG 349  
 Oy 352 S 352  
 Db 350 S 350

## RESULT 6

151199

activin beta B subunit - African clawed frog

C:Species: Xenopus laevis (African clawed frog)

C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999

C:Accession: 151199

R.Dohmann, C.E.; Hemmati-Brijvanlou, A.; Thomsen, G.H.; Fields, A.; Woolf, T.M.; Melt

Dev. Biol. 157, 474-483, 1993

A:Title: Expression of activin mRNA during early development in Xenopus laevis.

A:Reference number: 151199; MUID:93273083

A:Accession: 151199

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-370 &lt;DOH&gt;

A:Cross-references: GB:S61773; NID:g386027; PIDN:AAB26863.1; PID:g386028

C:Superfamily: Inhibin

Query Match

Best Local Similarity 32.7%; Score 607.5; DB 2; Length 370;

Matches 140; Conservative 70; Mismatches 122; Indels 51; Gaps 14;

Oy 5 LLAFLA--LAPTTVAATPRAGGCGPPTLEESORELLDLAKRSILDKLHILTORPT 62  
 Db 4 LLLPLLAGLAKTCAAPSPPTPRGCPSC--HPRMEDE---MLEAVKRHILTLHMQDRPN 57  
 Oy 63 LNPVSRAALFTALQHLHGVQALLEDNRECELSIFA---ETGLSTINOTRLDFHFSRDR 104  
 Db 58 ITHWVPRAAMVSALRKIHA--GRVREDGNLEIPDLDSLPPGHSSTENSAEITTFAPT 114  
 Oy 105 GLSTINOTRLDFHFSRDRACDRE--VQOASLMFVQPLPSNTTTLKRVLVLGPHN 159  
 Db 115 DDVVASVRRLSEFTIANE--GNQLTFVQSILMLYLKLEPVWDKSRKIRIRVHPODAFN 171  
 Oy 160 TNLTAQYLLFVDSASGWHOLPLGPEAQAACSG--HILTELVLEGQVAOSSVI-----L 212  
 Db 172 PDKNNWVEKKADIRSGHNTPTLTAIOSLPEBGERRLNLEVQCG--GGEYSVIVPYVDP 230  
 Oy 213 GGAHREPVAAVRVYG--GKHQIHRRGIDCGGSRMCCREFFVDREICGHMDITQREY 271  
 Db 231 GEESHREPLVVAHARLADNKRIRKRGLEDGHTNLCCROOFYIDRLIGMNDMIAPAGY 290  
 Oy 272 AMNFCIGCPHLHAGPGLIASFHTAVLNLKANTAAAGTTG--GSCCVPTARRPLSLLY 329  
 Db 291 YGNVCEGSCPAYLAGVPSASFSHTAVVNOYRMR--GLNPVTWSSCIPTKLSTWSMLY 347  
 Oy 330 YDRDSNIVKTDIPDMVVEAGCGS 352  
 Db 348 FDDEYNIVKRDVPMNIVDECGCA 370

## RESULT 7

S50899

betab Inhibin precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C:Date: 01-Aug-1995 #sequence\_revision 01-Sep-1995 #text\_change 17-Mar-1999

C:Accession: S50899

R:Thompson, D.A.; Cronin, C.N.; Martin, F.

Eur. J. Biochem. 226, 751-764, 1994

A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet

y DNase I footprinting.

A:Reference number: S50897; MUID:95112839

A:Accession: S50899

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-408 &lt;THO&gt;

A:Cross-references: EMBL:U16240

C:Genetics:

A:Insertions: 151/1

C:Superfamily: Inhibin

Query Match

Best Local Similarity 32.7%; Score 605; DB 2; Length 408;

Matches 145; Conservative 62; Mismatches 117; Indels 72; Gaps 15;

Oy 13 APTTVATPPA-----GQ---CPACGPTLEESOREL-----LIDLAKRSIL 52  
 Db 29 STPLPLPAAPPPPPPPGAGSGDPTSCG---FRPEELGRVDSDFLEAVKRRHL 84

QY 53 DKHLTORPTLNRPVSRALFTALQHLGVPQALLEDNR-----EDE 95  
 Db 85 NRQMRPRPNTTHAVPRAAMVATLRLKHA---GKVRGREGVEIPHLDSHSPGADQGERV 141  
 QY 96 CEIISFAETGLSTINQTRLDHFSSDRTAGDRE--VOQASIMFVQLPSNTWTI----- 148  
 Db 142 SEISFAETDGLASSRVLTFEFSNE---GNQNFVQASIMLYLKL---LPVLEKGR 195  
 QY 149 -KRVVLVGLRHN--TNLTATQYLLVEDASGWHOLPLGPEAOACSGHLLTLELVGCV 205  
 Db 196 KRVKRVYVQEGOGDGMVAVERKRLKSGMHTFPLETIALQALFSGERRSLDVGCD 255  
 QY 206 AQSIVL-----GCAHPRPVARVRVG-GKHQIRRGIDCGGSRMCROEFVDFRE 258  
 Db 256 CRELAVVPVVDPEESHSRPFVVOARLDGSRHRIKRGLECDRTNLCRCROFFIDFRL 315  
 QY 259 IGMHDMITQPEGYAMNFCIGCPPLHAGMPGIAAFHTAVLNLKANTAGTGG--GSC 316  
 Db 316 IGMNDMIAPTGYGNCCEGSCPAVLGVPGSASSHTAVVNOYRMR---GLNPQVNSC 372  
 QY 317 CVPTARRPLSLLYRDSNIVKTDIPDMVVEACGCS 352  
 Db 373 CIPTKLSTMSMLYFDEYNIVKRDVPMIVEEGCA 408

## RESULT 8

Inhibin beta-B chain precursor - human  
 N:Alternate names: activin AB chain B  
 C:Species: Homo sapiens (man)  
 C>Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text-change 01-Dec-2000  
 C:Accession: A40150; C24248; A40156; S10751  
 R:Mason, A.J.; Beremeler, L.M.; Schmelzer, C.H.; Schwall, R.H.  
 Mol. Endocrinol. 3, 1352-1358, 1989  
 A:Title: Activin B: precursor sequences, genomic structure and in vitro activities.  
 A:Reference number: A40150; MUID:90114200  
 A:Accession: A40150

A:Molecule type: DNA

A:Residues: 1-407 <MA5>

A:Cross-references: GB:M31668; GB:M31669; NID:g186419; PIDN:AAA59451.1; PID:g386827

R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.

Biochem. Biophys. Res. Commun. 135, 957-964, 1986

A:Title: Structure of two human ovarian Inhibins.

A:Reference number: A90123; MUID:86186863

A:Accession: C24248

A:Molecule type: mRNA

A:Residues: 55-407 <MA2>

A:Cross-references: GB:M31437; NID:g186416; PIDN:AAA59109.1; PID:g186417

R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.

Mol. Endocrinol. 3, 939-948, 1989

A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.

A:Reference number: A40156; MUID:89295443

A:Accession: A40156

A:Molecule type: mRNA

A:Residues: 22-46, 'A', 48-407 <FEN>

A:Cross-references: GB:M31632

A:Experimental source: testis

R:Schmelzer, C.H.; Burton, L.E.; Tamony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois, N.

Biochim. Biophys. Acta 1039, 135-141, 1990

A:Title: Purification and characterization of recombinant human activin B.

A:Reference number: S10751; MUID:90304183

A:Accession: S10751

A:Molecule type: Protein

A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 <SCH>

C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respectively.

C:Genetics:

A:Gene: GDB:INHBB

A:Cross-references: GDB:119347; OMIM:147390

A:Map position: 2cen-2q13

C:Superfamily: Inhibin

C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone

P:1-207domain; signal sequence #status predicted <SIG>

F:21-292/Domain: propeptide #status predicted <PRO>  
 F:293/Product: inhibin beta-B chain #status predicted <MAT>  
 F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

Best Local Similarity 32.4%; Score 599.5; DB 1; Length 407;

Matches 145; Conservative 60; Mismatches 118; Indels 73; Gaps 16;

QY 13 APTTAVTPRA-----GCG---CPACGPLELESOREL-----LIDLAKRSLID 53  
 Db 29 SPTPTPTPAAPPPPPPGSGSDTCTSCG---FRREELGRVGDLEAVKRHLIS 84  
 QY 54 KLHLTORPTLNRPVSRALFTALQHLGVPQALLEDNR-----EDQC 96  
 Db 85 NRQMRPRPNTTHAVPRAAMVATLRLKHA---GKVRGREGVEIPHLDSHSPGADQGERV 141  
 QY 97 EITISFAETGLSTINQTRLDHFSSDRTAGDRE--VOQASIMFVQLPSNTWTI----- 148  
 Db 142 SEISFAETDGLASSRVLTFEFSNE---GNQNFVQASIMLYLKL---LPVLEKGR 195  
 QY 149 KRVVLVGLRHN--TNLTATQYLLVEDASGWHOLPLGPEAOACSGHLLTLELVGCV 205  
 Db 196 KRVKRVYVQEGOGDGMVAVERKRLKSGMHTFPLETIALQALFSGERRSLDVGCD 254  
 QY 206 AQSIVL-----GCAHPRPVARVRVG-GKHQIRRGIDCGGSRMCROEFVDFRE 258  
 Db 256 CRELAVVPVVDPEESHSRPFVVOARLDGSRHRIKRGLECDRTNLCRCROFFIDFRL 314  
 QY 259 IGMHDMITQPEGYAMNFCIGCPPLHAGMPGIAAFHTAVLNLKANTAGTGG--GSC 316  
 Db 316 IGMNDMIAPTGYGNCCEGSCPAVLGVPGSASSHTAVVNOYRMR---GLNPQVNSC 371  
 QY 317 CVPTARRPLSLLYRDSNIVKTDIPDMVVEACGCS 352  
 Db 372 CIPTKLSTMSMLYFDEYNIVKRDVPMIVEEGCA 407

## RESULT 9

Inhibin beta-B chain precursor - rat  
 N:Alternate names: inhibin/activin beta B-chain  
 C:Species: Rattus norvegicus (Norway rat)  
 C>Date: 03-Apr-1992 #sequence, revision 01-Aug-1997 #text-change 16-Jul-1999  
 C:Accession: B41398; I53288; C40905  
 R:Feng, Z.M.; Li, Y.P.; Chen, C.L.C.  
 Mol. Endocrinol. 3, 1914-1925, 1989  
 A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit  
 A:Reference number: A41398; MUID:90190649  
 A:Accession: B41398

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 <FEN>

A:Cross-references: GB:M32756; GB:M32757; NID:g204943; PIDN:AAA41438.1; PID:g554460

R:Dykema, J.C.; Mayo, K.E.

Endocrinology 135, 702-711, 1994

A:Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin

A:Reference number: I53288; MUID:94307180

A:Accession: I53288

A:Molecule type: DNA

A:Residues: 1-7 <RES>

A:Cross-references: GB:S72477; NID:g619268

R:Esch, F.S.; Shimazaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno

Mol. Endocrinol. 1, 388-396, 1987

A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis

A:Reference number: A40905; MUID:90331931

A:Accession: C40905

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 133-411 <ESC>

C:Superfamily: Inhibin

Query Match

32.2%; Score 595.5; DB 2; Length 411;

Best Local Similarity 35.5%; Pred. No. 9.4e-46;  
Matches 139; Conservative 65; Mismatches 127; Indels 61; Gaps 12;

OY 13 APTTATPRA-----GQ---CPACGPTLEESQRL-----LIDLAKRSILD 53  
DB 29 SPTPPSPAPPPPPGAPGSGDITCTSCGGGGGFRPPELGVDFEAVKHHILS 29  
OY 54 KLHITQPTLNRPYSRAALRTALOHGVPQALLEDNR-----EQEC 96  
DB 89 RLQGRPRNTHAVPKAMVATLRLKLA---GKVEDGRVELPHLDGHSRGADGERS 145  
OY 97 EISFAETGLSTINQTRLDHFSSDRTAGDRE--VOQASLMFVQ-----LPSNTWTLK 149  
DB 146 EISFAETGLDGLASSRVLRYFFVSNE---GNQMLFVQASLMYLKLLPYLEKSGRRKRV 202  
OY 150 VRLVLVGHNTNLTLATQYLLEVDASGWHOLPLGEAOACSGHITLLELYEGOVAOSS 209  
DB 203 VKVYFOEGHGDNRNVVKKYDLKRSQWHTPITENIQALFERGERRLLDVQCDSCQEL 262  
OY 210 VIL-----GGAHRRPFAARVRG-GKHQIHRGIDCGGSMCCROEFVDFREIGWH 262  
DB 263 AVVEFVDPGSESHRPFFVVOARLDSDSRIRKRGLECGRTSLCCROQFDFRLIGWN 322  
OY 263 DMITOPGAYAMNFCIGQCPHIIAGMPGIAASFHTAVLNLKANTAGTTGG--GSCCVPT 320  
DB 323 DMITAPGTGYGNCGSCPAIAGVPGSASFHTAVNVOYRMR---GLNPGVNSCICPT 379  
OY 321 ARPLSLLYDRDSNIVKTDIPDMVVEACGS 352  
DB 380 KLSMSMLYFDDEYNIVKRDVPMNIVEECGA 411

# RESULT 10

Inhibin beta-B chain precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 01-Dec-2000  
C:Accession: A01394  
R:Masou, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Gullilemin, R.;  
Nature 318, 659-663, 1985  
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor  
A:Reference number: A83371; MUID:86092207  
A:Accession: A01394  
A:Molecule type: mRNA  
A:Residues: 1-349 <MAS>  
A:Cross-references: GB:X03267; NID:92005; PIDN:CAA27021.1; PID:92006  
C:Comment: The source of this protein is ovarian follicular fluid.  
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide  
different forms of inhibin have been isolated (A and B) that differ in the amino-terminal  
C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follicle  
stimulating hormone.  
C:Suprafamily: Inhibin  
C:Keywords: contraceptive; follicle stimulating hormone; glycoprotein; gonadotropin releasing hormone  
F.1-234/Domain: propeptide (fragment) #status predicted <PRO>  
F.235-349/Product: Inhibin beta-B chain #status predicted <MAT>  
F.35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 31.7%; Score 587; DB 1; Length 349;  
Best Local Similarity 37.7%; Pred. No. 4.4e-45;  
Matches 129; Conservative 62; Mismatches 109; Indels 42; Gaps 9;

OY 44 LDIKASILDKLHITQPTLNRPYSRAALRTALOHGVPQALLEDNR----- 92  
DB 17 LEAVKRIHLIRLQMRGPRNTHAVPKAMVATLRLKLA---GKVEDGRVELPHLDGHS 73  
OY 93 -----FOECETISFAETGLSTINQTRLDHFSSDRTAGDRE--VOQASLMFVQ----- 139  
DB 74 PGADGQERVELISFAETGLDGLASSRVLRYFFVSNE---GNQMLFVQASLMYLKLLPY 130  
OY 140 LPSNTWTLKLRVLVGHNTNLTLATQYLLEVDASGWHOLPLGEAOACSGHITLLE 199  
DB 131 LEKSGRRKRVAVKVVYFOEGHGDNRNVVKKYDLKRSQWHTPITENIQALFERGERRL 190  
OY 200 VLEGQVAOSSVIL-----GGAHRRPFAARVRG-GKHQIHRGIDCGGSMCCROQF 252

DB 191 DVQDCGQELAVFVDPGSESHRPFFVVOARLDSDSRIRKRGLECGRTSLCCROQF 250  
OY 253 FVDFREIGWHDMITOPGAYAMNFCIGQCPHIIAGMPGIAASFHTAVLNLKANTAGTTG 312  
DB 251 FIDRLIGWDMITAPGTGYGNCGSCPAIAGVPGSASFHTAVNVOYRMR---GLNPG 307  
OY 313 G--GSCCVPTARPLSLLYDRDSNIVKTDIPDMVVEACGS 352  
DB 308 GTVNSCICPTKLSMSMLYFDDEYNIVKRDVPMNIVEECGA 349

# RESULT 11

150103  
activin beta B - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C:Date: 13-Sep-1996 #sequence\_revision 13-Sep-1996 #text\_change 16-Jul-1999  
C:Accession: 150103  
R:Wiltbrodt, J.; Rosa, F.M.  
Genes Dev. 8, 1448-1462, 1994  
A:Title: Disruption of mesoderm and axis formation in fish by ectopic expression of a  
A:Reference number: 150103; MUID:95011555  
A:Accession: 150103  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-393 <WIT>  
A:Cross-references: EMBL:X76051; NID:9516356; PIDN:CAA53636.1; PID:9516357  
C:Genetics:  
A:Gene: Zactbetab  
C:Suprafamily: Inhibin

Query Match 31.0%; Score 573.5; DB 2; Length 393;  
Best Local Similarity 34.3%; Pred. No. 8.5e-44;  
Matches 134; Conservative 80; Mismatches 128; Indels 49; Gaps 14;

OY 1 MTSSLLAFLLAPTTATPRA---GQCPACGPTLEESQRL-----LIDLAKRSILDKLH 56  
DB 13 LVSTICIMCLISVOCSSLCAGTSGOESQCGSLGHQEDSGRMDTFLKVKRHLIRLO 72  
OY 57 LTQPTLNRPYSRAALRTALOHGVPQALLEDNR-----EQECETIS 100  
DB 73 MERPRITHTPIKAMVATLRLKLA---GKVEDGRVELPHLDGHSRGADGERS 129  
OY 101 FAETGLSTINQTRLDHFSSDRTAGDRE--VOQASLMFVQ-----LPSNTWTLKRVVLV 155  
DB 130 FASDDVPTSKSLYLLISNE---GNQMLYVLQANLMLYKLMPTGLEKLRKAVTVRVH 186  
OY 156 -----GPHNTNLTLATQYLLEVDASGWHOLPLGEAOACSGHITLLELYEGOVAOSSVI 211  
DB 187 SYEPGQNVHWPV-MEKREVELKRSQWHTPITENIQALFERGERRLDHIHCECEANV 245  
OY 212 L-----GGAHRRPFAARVRG-GKHQIHRGIDCGGSMCCROEFVDFREIGWH 263  
DB 246 LPLVDPSPSHRPFFVVOARLDSDSRIRKRGLECGRTSLCCROQFDFRLIGWN 305  
OY 264 WITOPGAYAMNFCIGQCPHIIAGMPGIAASFHTAVLNLKANTAGTTGG--GSCCVPTA 321  
DB 306 WITAPGTGYGNCGSCPAIAGVPGSASFHTAVNVOYRMR---GLNPGVNSCICPTK 362  
OY 322 RRELSLLYDRDSNIVKTDIPDMVVEACGS 352  
DB 363 LSTMSMLYFDDEYNIVKRDVPMNIVEECGA 393

# RESULT 12

WFGGBA  
Inhibin beta-A chain precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 18-Jun-1999  
C:Accession: A01393  
R:Masou, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Ueno, N.; Ying, S.Y.; Gullilemin, R.  
Nature 318, 659-663, 1985  
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor



A:Reference number: A9371; MUID:86092207  
 A:Accession: A01393  
 A:Molecule type: mRNA  
 A:Residues: 1-424 <MAS>  
 A:Cross-references: GB:X03266; NID:92002; PIDN:CAA27020.1; PID:92003  
 C:Comment: The source of this protein is ovarian follicular fluid.  
 C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide  
 C:Comment: The mature protein has been isolated (A and B) that differ in the amino-terminal  
 C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follicle  
 C:Suprafamily: Inhibin  
 C:Keywords: contraceptive; follicle tropin inhibitor; glycoprotein; gonad  
 F:1-20/Domain: signal sequence #status predicted <SIG>  
 F:21-308/Domain: propeptide #status predicted <PRO>  
 F:309-424/Product: inhibin beta-A chain #status predicted <MAT>  
 F:165/Binding site: carboxylate (Asn) (covalent) #status predicted

Query Match 30.4%; Score 562; DB 1; Length 424;  
 Best Local Similarity 31.2%; Pred. No. 1e-42;  
 Matches 131; Conservative 69; Mismatches 142; Indels 78; Gaps 10;

OY 6 LAFLLAPPTVTPRAG-----QCPACGPTL--ELESORELLDLAKRSILDRLHT 58  
 DB 10 LASCWITVSSPTPGSGHSAAPDCSCALATLPKDPVNSQPEVAVKHHILMLHLK 69  
 OY 59 QPPTLRPVSRALRFLALH-----GVPQALLDNRQECETISFAET 104  
 DB 70 KRDPVQPPVKALLNAIRKLHVKGKGVENGVELEDIGRAENNELMEQTSITFAEA 129  
 OY 105 GLSTINOTRLDFHSSDRTAGDRE--VOQASLMFVQLPSTNTWT-LKVVVLG----- 156  
 DB 130 GTA-----RKTLEFISKEGSDLSVERAEWLFKVPKANRTTKYSIRLFQOORRPG 184  
 OY 157 -----PHNTNLTAQYLLVDASGMHQLPLGPEAQ-----AAC 190  
 DB 185 SADAGEAEADVPEEKSEVLLSEKVDARKSTWHLFPVSSIORLLDQKSLDTRAC 244  
 OY 191 SOGHILT-LELVLEGVQVQSSVILG-----AAHRRPFAARVGVGK--HQ 232  
 DB 245 ECHGEGALVLLGKKKKKEEAEGRGEGAGVDEKQSHRRPFLMLQARSEEHPR 304  
 OY 233 IHRRCIDCGGSRMCROEFVDFREIGHMDWITOPEGYAMNFCIGCPPLHAGMPGIA 292  
 DB 305 RRRRGLECDGKVNICKKQFVSKDIGMDWITAPSGHANVCCEGCPSHIATGSSSL 364  
 OY 293 SPHTAVNLKNTAAGTTGGSCCVPFARPLSLLYRDSNIYKTDIPDMVVEACGCS 352  
 DB 365 SPHTAVNLKNTAAGTTGGSCCVPFARPLSLLYRDSNIYKTDIPDMVVEACGCS 424

## RESULT 13

S31440

Inhibin beta-A chain - mouse  
 N:Alternate names: activin A; mesoderm-inducing factor WEHI-MIF  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999  
 C:Accession: A60087; 148265; S31440  
 R:Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack, J.M.  
 Development 110, 435-443, 1990  
 A:Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia cell  
 A:Reference number: A60087; MUID:92155098  
 A:Accession: A60087  
 A:Molecule type: protein  
 A:Residues: 309-311, 'X', 313-318, 'XX', 321-325 <AL2>  
 R:Albano, R.M.; Groome, N.; Smith, J.C.  
 Development 117, 711-723, 1993  
 A:Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cells  
 A:Reference number: 148243; MUID:93321614  
 A:Accession: 148265  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-424 <RES>  
 A:Cross-references: EMBL:X69619; NID:950145; PIDN:CAA4325.1; PID:950146  
 C:Suprafamily: Inhibin

Query Match 30.2%; Score 559; DB 1; Length 424;  
 Best Local Similarity 32.1%; Pred. No. 1.9e-42;  
 Matches 135; Conservative 71; Mismatches 135; Indels 80; Gaps 12;

OY 6 LAFLLAPPTVTPRAG-----QCPACGPTLE--SORELLDLAKRSILDRLHT 57  
 DB 10 LASCWITVSSPTPGSGHSAAPDCSCALATLPKDPVNSQPEVAVKHHILMLHLK 68  
 OY 58 TORPTLRPVSRALRFLALH-----GVPQALLDNRQECETISFAE 103  
 DB 69 KRDPVQPPVKALLNAIRKLHVKGKGVENGVELEDIGRAENNELMEQTSITFAEA 128  
 OY 104 TGLSTINOTRLDFHSSDRTAGDRE--VOQASLMFVQLPSTNTWT-LKVVVLGPR-- 158  
 DB 129 SGT-----RKTLEFISKEGSDLSVERAEWLFKVPKANRTTKYSIRLFQOORRPG 183  
 OY 159 -----NTNLTAQYLLVDASGMHQLPLGPEAQASOGHILTLELVLE 202  
 DB 184 GSDTGDDEAEEMKLGERSLLSEKVDARKSTWHLFPVSSIORLLDQKSLDTRIA 243  
 OY 203 GOVAQSS-----VILG-----GAHRRP--VAARVGVGKII 231  
 DB 244 ECHGEGALVLLGKKKKKEVDGDKKKDSDGLEEKQSHRRPFLMLQARQSEEDHP 303  
 OY 232 IHRRCIDCGGSRMCROEFVDFREIGHMDWITOPEGYAMNFCIGCPPLHAGMPGIA 291  
 DB 304 RRRRGLECDGKVNICKKQFVSKDIGMDWITAPSGHANVCCEGCPSHIATGSSSS 363  
 OY 292 ASHTAVNLKNTAAGTTGGSCCVPFARPLSLLYRDSNIYKTDIPDMVVEACGCS 351  
 DB 364 LSFHTVNIHYRMGRHSPANLKSQCVPTKLRPMMLYDDGQNIKKDIONMIVECGC 423  
 OY 352 S 352  
 DB 424 S 424

## RESULT 14

B24248

Inhibin beta-A chain precursor (validated) - human  
 N:Alternate names: activin A; activin AB chain A; erythroid differentiation factor; m  
 C:Species: Homo sapiens (man)  
 C:Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 08-Dec-2000  
 C:Accession: S30488; B23556; B24248; A30884; S33551; P00010  
 R:Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukumizu, A.  
 DNA Seq. 2, 103-110, 1991  
 A:Title: Structure and sequence analysis of the human activin beta(A) subunit gene.  
 A:Reference number: S30488; MUID:92135888  
 A:Accession: S30488  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-426 <TAN>  
 A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA40805.1; PID:9825621  
 A:Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residu  
 R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.  
 FEBS Lett. 206, 329-334, 1986  
 A:Title: Human inhibin genes. Genomic characterisation and sequencing.  
 A:Reference number: A91366; MUID:87005283  
 A:Accession: B23556  
 A:Molecule type: DNA  
 A:Residues: 311-426 <STE>  
 A:Cross-references: GB:X04447; NID:933928; PIDN:CAA28041.1; PID:933929  
 R:Masson, A.J.; Niall, H.D.; Seeburg, P.H.  
 Biochem. Biophys. Res. Commun. 135, 957-964, 1986  
 A:Title: Structure of two human ovarian inhibins.  
 A:Reference number: A90123; MUID:86186863  
 A:Accession: B24248  
 A:Molecule type: mRNA  
 A:Residues: 1-426 <MAS>  
 A:Cross-references: GB:M13436; NID:9186414; PIDN:AAA59168.1; PID:9307069  
 R:Murata, M.; Eto, Y.; Shibata, H.; Sakai, M.; Muramatsu, M.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988

A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the inh  
A:Reference number: A30884; MUID:88190086  
A:Accession: A30884  
A:Molecule type: mRNA  
A:Residues: 1-426 <MUR>  
A:Cross-references: GB:03634; NID:g181946; PIDN:AAA35787.1; PID:g181947  
R:Berger, H.; Walter, M.; Northmann, W.  
submitted to the EMBL Data Library, April 1993  
A:Description: Nucleotide sequence coding for the mature subunit beta(A) of human inhibi  
A:Reference number: S3351  
A:Accession: S3351  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 311-376, 'AC', 380-426 <BER>  
A:Cross-references: EMBL:X72498; NID:g297786; PIDN:CAA51163.1; PID:g755740  
R:Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda, T.; Matsuzaki, H.; Hirose,  
Biochem. Biophys. Res. Commun. 174, 1163-1168, 1991  
A:Title: Purification of megakaryocyte differentiation activity from a human fibrous tis  
A:Reference number: P0010; MUID:91144591  
A:Accession: P0010  
A:Molecule type: protein  
A:Residues: 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 <PU>  
C:Comment: Activin A and B are homodimers of inhibin beta-A or inhibin beta-B, respecti  
bin beta-A and beta-B, respectively.  
C:Genetics:  
A:Gene: GDB:INHBA  
A:Cross-references: GDB:119346; OMIM:147290  
A:Map position: 7p15-7p13  
A:Introns: 129/3  
C:Superfamily: Inhibin  
C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-310/Domain: propeptide #status predicted <PRO>  
F:311-426/Product: inhibin beta A chain #status experimental <MAT>  
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 557; DB 1; Length 426;  
Best Local Similarity 31.5%; Pred. No. 2, 9e-42;  
Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12;

QY 6 LIAFLLAFTVATPRAG-----QCPACGGPTL--ELSORELLDLAKSTIDKILHT 58  
DB 10 LLAACMIIVRSSPTPGSEGHSAAPDCPSALALPKDVPNSQPEMVAVKHILMLHLK 69  
QY 59 QRPFLNRPVSRALRTALQHLH-----GVPGALLEDRKEDCEITISFAET 104  
DB 70 KRPDVTPQPKAALLNAIRKLHGVKGVENGVEIEDIGRAEMNELMEQTSIITFAES 129  
QY 105 GLSTINQTRLDPHFSSDRTAGDRE--VOQASLMFVQLP--SNTTWT--LKVRVVLGPH--- 158  
DB 130 GTA-----KRTLHFEISKESGSDLSVERAEVWLFLKVPKANRTKTYIRLRFQOQKHOG 184  
QY 159 -----NTNLTLATQYLLEVDASGWHQQLPLGPEAQACSGHILTELVLEG 203  
DB 185 SLDTGEAEAEVGLKGESEMLISEKVVDARKSTWHVFPVSSIQRLDQSGSSLDVRIAC 244  
QY 204 QVAQSS---VILG-----GA-----AHRPF--VAARVAVGSK 230  
DB 245 EGOQEGASLVLLGKKKKKEEGEGKKKGEGGAGADEKEQSHRPFMLQAROSEDPH 304  
QY 231 HQHNRGIDQGGSRKCCREDFVDREIGHWMDITQEGYAMNFCIGCPHLIGMPGI 290  
DB 305 HRRRRRLKEDGVNICKKOPFVSPKIDGNMDWIIASGHNANCEECESHIAGTSGS 364  
QY 291 AASFHTAVLNLKANTAAAGTGGCCGCPVAFRRPLSLLYVRDSNIIVTDDIPDMVVEAG 350  
DB 365 SLSPHSVIVIHNRKRGHSFPAKLNKSCCPTKLRPMKMLYDDGCONIKKDIOMNIVEEGG 424

## RESULT 15

S50898

Inhibin beta-A chain precursor - bovine  
N:Alternate names: activin; mesoderm inducing factor  
C:Species: Bos primigenius taurus (cattle)  
C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 10-Sep-1999  
C:Accession: S50898; B25732; A60960; B61548  
R:Thompson, D.A.; Cronin, C.N.; Martin, F.  
Eur. J. Biochem. 226, 751-764, 1994  
A:Title: Genomic cloning and sequence analyses of the bovine alpha-, beta(A)- and bet  
A:Reference number: S50897; MUID:95112839  
A:Accession: S50898  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-425 <THO>  
A:Cross-references: EMBL:U16238  
R:Porage, R.G.; Ring, J.M.; Brown, R.W.; McInerney, B.V.; Cobon, G.S.; Gregson, R.P.;  
Proc. Natl. Acad. Sci. U.S.A. 83, 3091-3095, 1986  
A:Title: Cloning and sequence analysis of cDNA species coding for the two subunits of  
A:Reference number: A94097; MUID:86205842  
A:Accession: B25732  
A:Molecule type: mRNA  
A:Residues: 258-425 <FOR>  
A:Cross-references: GB:M3274; NID:g163196; PIDN:AAA97415.1; PID:g163197  
A:Note: part of this sequence, including the amino end of the mature protein, was con  
R:Chertov, O.Y.; Krasnosel'skii, A.L.; Bogdanov, M.E.; Hoperskaya, O.A.  
Biomed. Sci. 1, 499-506, 1990  
A:Title: Mesoderm-inducing factor from bovine amniotic fluid: purification and N-term  
A:Reference number: A60960; MUID:92126853  
A:Accession: A60960  
A:Molecule type: protein  
A:Residues: 310-312, 'X', 314-319, 'XX', 322-328, 'P' <CH>  
R:Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Mats  
Mol. Cell. Endocrinol. 44, 55-60, 1986  
A:Title: Isolation of bovine follicular fluid inhibin of about 32 kDa.  
A:Reference number: A61548; MUID:86136989  
A:Accession: B61548  
A:Molecule type: protein  
A:Residues: 310-313 <PUK>  
C:Genetics:  
A:Introns: 130/1  
C:Superfamily: Inhibin  
C:Keywords: disulfide bond; glycoprotein; gonad; heterodimer; homodimer; hormone  
F:1-28/Domain: signal sequence #status predicted <SIG>  
F:29-309/Domain: propeptide #status predicted <PRO>  
F:310-425/Product: beta-A inhibin/activin #status experimental <MAT>  
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 30.1%; Score 556.5; DB 1; Length 425;  
Best Local Similarity 31.1%; Pred. No. 3, 2e-42;  
Matches 131; Conservative 76; Mismatches 135; Indels 79; Gaps 11;

QY 6 LIAFLLAFTVATPRAG-----QCPACGGPTL--ELSORELLDLAKSTIDKILHT 58  
DB 10 LLAACMIIVRSSPTPGSEGHSAAPDCPSALALPKDVPNSQPEMVAVKHILMLHLK 69  
QY 59 QRPFLNRPVSRALRTALQHLH-----GVPGALLEDRKEDCEITISFAET 104  
DB 70 KRPDVTPQPKAALLNAIRKLHGVKGVENGVEIEDIGRAEMNELMEQTSIITFAES 129  
QY 105 GLSTINQTRLDPHFSSDRTAGDRE--VOQASLMFVQLP--SNTTWT--LKVRVVLGPH--- 158  
DB 130 GTA-----KRTLHFEISKESGSDLSVERAEVWLFLKVPKANRTKTYIRLRFQOQKHOG 184  
QY 159 -----NTNLTLATQYLLEVDASGWHQQLPLGPEAQACSGHILTELVLEG 203  
DB 185 SLDTGEAEAEVGLKGESEMLISEKVVDARKSTWHVFPVSSIQRLDQSGSSLDVRIAC 244  
QY 204 QVAQSS---VILG-----GA-----AHRPF--VAARVAVGSK 231  
DB 245 EGOQEGASLVLLGKKKKKEEGEGKKKGEGGAGADEKEQSHRPFMLQAROSEDPH 304

Tue Oct 15 13:49:40 2002

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Search completed: October 12, 2002, 02:09:55  
Job time : 29 secs

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OM protein - protein search, using sw model

Run on: October 11, 2002, 22:35:53 : Search time 13.5 seconds  
(without alignments)  
1009.576 Million cell updates/sec

Title: US-09-684-383-2

Perfect score: 1849  
Sequence: 1 MTSLLAFLLAPTTATP.....DSNVKTDIPDMVENCSCS 352

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: SwissProt\_40:\*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1849	100.0	352 1	IHBC_HUMAN
2	1392	75.3	352 1	IHBC_MOUSE
3	1379.5	74.6	351 1	IHBC_RAT
4	664	35.9	350 1	IHBE_HUMAN
5	648	35.0	350 1	IHBE_MOUSE
6	647	35.0	350 1	IHBE_RAT
7	605	32.7	408 1	IHBB_BOVIN
8	599.5	32.4	407 1	IHBB_HUMAN
9	598	32.3	391 1	IHBB_CHICK
10	587	31.7	349 1	IHBB_PIG
11	562	30.4	424 1	IHBA_PIG
12	561	30.3	424 1	IHBA_RAT
13	560	30.3	426 1	IHBA_HORSE
14	559	30.2	424 1	IHBA_MOUSE
15	557	30.1	426 1	IHBA_HUMAN
16	556.5	30.1	425 1	IHBA_BOVIN
17	552.5	29.9	425 1	IHBA_SHEEP
18	527	28.5	424 1	IHBA_CHICK
19	476	25.7	255 1	IHBB_MOUSE
20	305.5	16.5	405 1	GDFF_MOUSE
21	304.5	16.5	407 1	GDFF_HUMAN
22	284.5	15.4	393 1	BMP2_RAT
23	284	15.4	396 1	BMP2_HUMAN
24	283	15.3	394 1	BMP2_MOUSE
25	281	15.2	374 1	GDFF_BRARE
26	271.5	14.7	395 1	BMP2_RABIT
27	270	14.6	395 1	GDFF_BOVIN
28	270	14.6	396 1	BMP2_DAMPA
29	267	14.4	357 1	GDFF_MOUSE
30	267	14.4	375 1	GDFF_SHEEP
31	264	14.3	375 1	GDFF_PIG
32	261	14.1	375 1	GDFF_HUMAN
33	261	14.1	376 1	GDFF_MOUSE

34	261	14.1	398 1	BMP4_XENLA	P30884 xenopus lae
35	259	14.0	375 1	GDFF_PAPIA	O18828 papio hamed
36	257	13.9	375 1	GDFF_MELGA	O42221 melalegris 9
37	256.5	13.9	376 1	GDFF_RAT	O35312 ratius norv
38	256	13.8	375 1	GDFF_CHICK	O42220 gallus gall
39	253	13.7	372 1	GDFF_HUMAN	P27539 homo sapien
40	247	13.4	345 1	GDFF_RAT	O92117 ratius norv
41	246.5	13.3	353 1	BMP2_CHICK	O90751 gallus gall
42	246	13.3	398 1	BMP4_XENLA	P25703 xenopus lae
43	241.5	13.1	355 1	DYR1_BRARE	P35621 brachydanio
44	240.5	13.0	399 1	BMP4_MOUSE	P34821 mus musculu
45	240	13.0	408 1	BMP4_DAMPA	O29607 dama dama (

## ALIGNMENTS

RESULT 1  
ID IHBC\_HUMAN STANDARD: PRT: 352 AA.  
AC P55103;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Inhibin beta C chain precursor (Activin beta C chain).  
GN IHBC.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95126961; PubMed=7826378;  
RA Hoeten G., Neidhardt H., Schneider C., Pohl J.;  
RT "Cloning of a new member of the TGF-beta family: a putative new  
RT activin beta C chain."  
RT Biochem. Biophys. Res. Commun. 206:608-613(1995).  
RN [2]  
RP TISSUE SPECIFICITY.  
RX MEDLINE=98089987; PubMed=9428386;  
RA Thomas T.Z., Chapman S.M., Hong W., Gursingfne C., Mellor S.L.,  
RA Fletcher R., Pedersen J., Risbridger G.P.;  
RT "Inhibins, activins, and follistatins: expression of mRNAs and  
RT cellular localization in tissues from men with benign prostatic  
RT hyperplasia."  
RT Prostate 34:34-43(1998).  
CC -I- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
CC RESECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
CC ACTIVINS.  
CC -I- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
CC SIMILARITY).  
CC -I- TISSUE SPECIFICITY: EXPRESSED IN BENIGN PROSTATIC HYPERPLASIA.  
CC -I- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
CC EMBL: X82540; CAA57890.1; .



Query Match 75.3%, Score 1392; DB 1; Length 352;  
 Best Local Similarity 75.9%, Pred. No. 1.7e-119;  
 Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;

1 MTSSLLAFLLAPTTVPTRAGCGCPGLEESORELLDLAKSIIDKLHNTOR 60  
 1 MASSLLALLLTPTTVNPKTEGPCPCGALPDESORELLDLAKSIIDKLHNTOR 60  
 61 PTLNRPVSRALRTALQHLHVPQALGE-DNREOCEIISFAETGISTINOTRLDFHFS 119  
 61 PILSRPVSRGALKTALQHLHVPQALGE-DNREOCEIISFAETGISTINOTRLDFHFS 120  
 120 SDRTAGDREVOQASLMFVQVLPSTNTWLKRVLYLCPHNTNLTATQYLLLEVADSGMHO 179  
 121 G-RMAASGMEVQTRFEMFQFPHNATQTNIRVLYLPRYDTNLTLSQYVQVNASGMQ 179  
 180 LPLGPEAQAACSGHLLTLEVLGQAQSSVILGGAHNPFAARVAVRGKRGHHRGID 239  
 180 LPLGPEAQAACSGHLLTLEVLGQAQSSVILGGAHNPFAARVAVRGKRGHHRGID 239  
 240 CGGSRMCCROEFFVDFRIGMDWIIIOPEGYAMNFCIGCPHIGMPCIASFHTAVL 299  
 240 CGGSRMCCROEFFVDFRIGMDWIIIOPEGYAMNFCIGCPHIGMPCIASFHTAVL 299  
 300 NLKANTAGTTGGSCCVPFARRPLSLLYDRDSNIVKTDIPDMVEACGCS 352  
 300 NLKANTAGTTGGSCCVPFARRPLSLLYDRDSNIVKTDIPDMVEACGCS 352

RESULT 3  
 ID HBC RAT STANDARD: PRT: 351 AA.

AC 09MUK5:  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Inhibin beta C chain precursor (Activin beta-C chain).  
 GN INHBC.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;  
 OC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar.  
 RA Rossmuth W., Peter B., Schulte-Hermann R.;  
 RT "Ret activin beta C and beta E: sequence and expression."  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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DR EMBL: AF140031; AD30132.1;  
 DR HSSP: P18075; 1BMP.  
 DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR001318; Inhibin\_beta.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIBINA.  
 DR PRINTS: PR00672; INHIBINB.  
 DR PRINTS: PR000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA\_1; 1.  
 KW Growth factor; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 18  
 FT PROPEP 19 236  
 FT CHAIN 237 351  
 FT DISULFID 239 246  
 FT DISULFID 246 316  
 FT DISULFID 275 348  
 FT DISULFID 279 350  
 FT DISULFID 315 315  
 FT CARBOHYD 110 110  
 FT CARBOHYD 142 142  
 FT CARBOHYD 160 160  
 SO SEQUENCE 351 AA; 39335 MW; 6B219BF6C3E180A1 CRC64;

Query Match 74.6%, Score 1379.5; DB 1; Length 351;  
 Best Local Similarity 75.6%, Pred. No. 2.4e-118;  
 Matches 266; Conservative 30; Mismatches 55; Indels 1; Gaps 1;

1 MTSSLLAFLLAPTTVPTRAGCGCPGLEESORELLDLAKSIIDKLHNTOR 60  
 1 MASSLLALLLTPTTVNPKTEGPCPCGALPDESORELLDLAKSIIDKLHNTOR 60  
 61 PTLNRPVSRALRTALQHLHVPQALGE-DNREOCEIISFAETGISTINOTRLDFHFS 120  
 61 PILSRPVSRGALKTALQHLHVPQALGE-DNREOCEIISFAETGISTINOTRLDFHFS 119  
 121 DRTAGDREVOQASLMFVQVLPSTNTWLKRVLYLCPHNTNLTATQYLLLEVADSGMHO 180  
 120 DRTAGDREVOQASLMFVQVLPSTNTWLKRVLYLCPHNTNLTATQYLLLEVADSGMHO 179  
 180 LPLGPEAQAACSGHLLTLEVLGQAQSSVILGGAHNPFAARVAVRGKRGHHRGID 240  
 180 LPLGPEAQAACSGHLLTLEVLGQAQSSVILGGAHNPFAARVAVRGKRGHHRGID 239  
 241 CGGSRMCCROEFFVDFRIGMDWIIIOPEGYAMNFCIGCPHIGMPCIASFHTAVL 300  
 240 CGGSRMCCROEFFVDFRIGMDWIIIOPEGYAMNFCIGCPHIGMPCIASFHTAVL 299  
 301 LKANTAGTTGGSCCVPFARRPLSLLYDRDSNIVKTDIPDMVEACGCS 352  
 300 LKANTAGTTGGSCCVPFARRPLSLLYDRDSNIVKTDIPDMVEACGCS 351

RESULT 4

ID HBE HUMAN STANDARD: PRT: 350 AA.

AC P58166;  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DE Inhibin beta E chain precursor (Activin beta-E chain).  
 GN INHBE.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Rhadowyosarcoma;  
 RA Strausberg R.;  
 RL Submitted (Mar-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.

CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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DR EMBL: BC005161; AAH05161.1; -  
 DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR001318; Inhibin\_betaC.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIBIN.  
 DR PRINTS: PR00672; INHIBIN.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA\_1; 1.  
 DR Growth factor; Hormone; Glycoprotein; signal.  
 KM SIGNAL 1 19  
 FT PROPEP 237 350  
 FT CHAIN 237 350  
 FT DISULFID 240 248  
 FT DISULFID 247 315  
 FT DISULFID 247 315  
 FT DISULFID 280 349  
 FT DISULFID 314 349  
 FT CAROHD 198 198  
 SO SEQUENCE 350 AA; 38561 MW; A49C1495677E3BE6F CRC64;

Query Match 35.9%; Score 664; DB 1; Length 350;  
 Best Local Similarity 43.3%; Pred. No. 4.3e-53;  
 Matches 156; Conservative 52; Mismatches 118; Indels 34; Gaps 14;

OY 9 FULLAFTVATPRAGGOCPCAGPPTLEESORELLDLAKSLDKLHUTQPTLNRPVS 68  
 DB 9 WLVLLWALVRAOGTGVSCGSKLAPQAEALVLELAKQDIDGLHUTSRPTTHPP 68  
 OY 69 RAALRTALOHGCVPGALGLEDNREDECEIISFAE-TGLSTINGTRDLPFSSDPTAGDR 127  
 DB 69 QALTRALRLRQ---PGSVAPNGE---EVIISFATVTDSTSAVSSLLFHLSTPRS--M<sup>1</sup>119  
 OY 128 EVQOASLIMFYOLPSNTTMTLKVRLVLP---HNTNLTLATQYLEVDASGMQLPGLC 183  
 DB 120 HLYHARLMLHV-LPT-LPTGLCTIRFGWRRRRGGRTLLAEHHTML---GMHTLTLP 174  
 OY 184 PEAGACSGGHLLEL---VLEGO---VAOSSVILGGAH-RPFAVARVVG--GKHQIH 234  
 DB 175 SSGGEGKSGKLTQIDCRPLENSVTGPPRLLDTPAGHOQPLELTKRNEPAGRAR 234  
 OY 235 RRGIDCGGSMCCRGFEVDFREIGWHDIIQPEGYAMNECICGCPHLHIGMPGIAASF 294  
 DB 235 RRTPTCEPATPLCCRDHYVDFQELGWRWILQPEGYQVANCSCGCPHLHIGMPGIAASF 294  
 OY 295 HTAVNLTKANT--AAGTGGGGCCVPTARRPLSLYYDRSDNIKTDIPMVEACGCS 352  
 DB 295 HSAVSFLKANNPWPAST-----SCVPTARRPLSLLYLDHNGVNVKTDVPMVEACGCS 350

RESULT 5  
 ID INBE\_MOUSE STANDARD; PRT; 350 AA.  
 AC 008717;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta E chain precursor (Activin beta-E chain).  
 GN INBE.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 CC NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC Tissue-Liver:  
 RX MEDLINE-97096313; PubMed-8941337;  
 RA Fang J., Yin W., Smiley E., Bonadio J.;  
 RT "Molecular cloning of the mouse activin beta E subunit gene";  
 RL Biochem. Biophys. Res. Commun. 228:669-674(1996).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-97224404; PubMed-9070865;  
 RA Fang J., Wang S.O., Smiley E., Bonadio J.;  
 RT "Genes coding for mouse activin beta C and beta E are closely linked  
 RT and exhibit a liver-specific expression pattern in adult tissues";  
 RL Biochem. Biophys. Res. Commun. 231:655-661(1997).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- DEVELOPMENTAL STAGE: FIRST EXPRESSION IN EMBRYONIC LIVER IS  
 CC DETECTED AT DAY E17.5.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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DR EMBL: U96386; AAB53801.1; -  
 DR HSSP: P12643; 38MP.  
 DR MCD; MGI:109269; Inbe.  
 DR InterPro: IPR002400; GF\_cysknol.  
 DR InterPro: IPR001318; Inhibin\_betaC.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00436; GF\_CYSKNOT.  
 DR PRINTS: PR00672; INHIBINBC.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA\_1; 1.  
 KM Growth factor; Hormone; Glycoprotein; signal.  
 FT SIGNAL 1 21  
 FT PROPEP 22 236  
 FT CHAIN 237 350  
 FT DISULFID 240 248  
 FT DISULFID 247 315  
 FT DISULFID 276 347



FT DISULFID 280 349 BY SIMILARITY.  
 FT DISULFID 314 314 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 350 AA: F37C76C8061D8AD9 CRC64:

Query Match 35.0%; Score 648; DB 1; Length 350;  
 Best Local Similarity 42.4%; Pred. No. 1.2e-51;  
 Matches 153; Conservative 58; Mismatches 118; Indels 32; Gaps 14;

QY 6 LIAFLLLPTVATPRAGCCGCGPTLEESQRELLDLAKRSITDKLHTORPTLNR 65  
 8 LMTLLMALWVQSRSA--CPSCGPTLPQGERALVLELAKQQLLEGILHSRPRTR 65  
 DB 66 PVSRALRTALQHLGVPGALLDRECECEIISFA--ETGLSTINOTRLDHFSSDR 122  
 66 PLPQALTRALRLQ--PK-SNVPGRNRE---KVISFATIDKSTYSY-RSMLEFOLS--- 115  
 QY 123 TAGDREVOQASLMFFVOLPSNTTWLTKVNLVLPHTNLTLATQYLL--VDASGMHOL 180  
 116 PLMSHNLVHARL--WLHVPRSPGTLYLIRFCG--TTRCGSRFTLAHQTTSSGMHAL 171  
 DB 181 PLGPEAOACSGCHLTLELVLEGOVAOSS-----VILGAA-HRPFVARVAVG--GKH 231  
 172 TLPSGLNSEDSGVYKQLERPRPLDLNSTAAGLPRLLDLTAQOQRPFLKIRANEPGAG 231  
 QY 232 QIHRGIDCGGSRMCCROEFVDREIGMHDIIOPEGYAMNFCIGCPPLHAGMPCIA 291  
 232 RARRRTPCESEPTLCCRDHYVDQELGMRDITLOPEGYOLNCGGCPPLHAGSPGIA 291  
 DB 292 ASFTAVLNLKANTAACTGGSCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGC 351  
 292 ASFTAVLNLKANTAACTGGSCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGC 351  
 QY 352 S 352  
 DB 350 S 350

RESULT 6  
 ID INBE\_RAT STANDARD: PRT: 350 AA.  
 AC 088959: QGR285;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta E chain precursor (Activin beta-E chain).  
 GN INBE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN 11  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver, and Lung;  
 RX MEDLINE=20290891; PubMed=10828834;  
 RA O'Bryan M.K., Sedore K.L., Gerdpraseert O., Hedger M.P., Hearn M.T.W.,  
 RA de Kretser D.M.;  
 RT "Cloning and regulation of the rat activin betaE subunit.";  
 RL J. Mol. Endocrinol. 24:409-418(2000).  
 RN 12  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar; Peter B., Schulte-Hermann R.;  
 RA Rossmann W.;  
 RT "Rat activin beta C and beta E: sequence and expression.";  
 RL Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLICULOPHILIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF

CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF089825; AAC36741.1;  
 CC EMBL: AF140032; AAD30133.1;  
 CC HSP: P12643; 3BP.  
 CC Interpro: IPR002400; GF\_cysknob.  
 CC Interpro: IPR001318; Inhibin\_betaC.  
 CC Interpro: IPR001839; TGF-beta.  
 CC Pfam: PF00019; TGF-beta; 1.  
 CC PRINTS: PR00438; GFCYSKNOT.  
 CC PRINTS: PR00672; INHIBINBC.  
 CC PRODOM: PD000357; TGF-beta; 1.  
 CC SMART: SM00204; TGFB; 1.  
 CC PROSITE: PS00250; TGF-BETA; 1.  
 CC Growth factor; Hormone; Glycoprotein; Signal.  
 CC SIGNAL 1  
 CC PROPEP 22 236  
 CC CHAIN 237 350  
 CC INHIBIN BETA E CHAIN.  
 CC FT DISULFID 240 248 BY SIMILARITY.  
 CC FT DISULFID 247 315 BY SIMILARITY.  
 CC FT DISULFID 276 347 BY SIMILARITY.  
 CC FT DISULFID 280 349 BY SIMILARITY.  
 CC FT DISULFID 314 314 INTERCHAIN (BY SIMILARITY).  
 CC FT CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 CC FT CONFLICT 160 161 EH -> DY (IN REF. 2).  
 SO SEQUENCE 350 AA: 38698 MW: 0CBF6E108E26E3 CRC64:

Query Match 35.0%; Score 647; DB 1; Length 350;  
 Best Local Similarity 42.4%; Pred. No. 1.5e-51;  
 Matches 153; Conservative 55; Mismatches 121; Indels 32; Gaps 14;

QY 6 LIAFLLLPTVATPRAGCCGCGPTLEESQRELLDLAKRSITDKLHTORPTLNR 65  
 8 LMTLLMALWVQSRSA--CPSCGPTLPQGERALVLELAKQQLLEGILHSRPRTR 65  
 DB 66 PVSRALRTALQHLGVPGALLDRECECEIISFA--ETGLSTINOTRLDHFSSDR 122  
 66 PLPQALTRALRLQ--PK-SNVPGRNRE---KVISFATIDKSTYSY-RSMLEFOLS--- 115  
 QY 123 TAGDREVOQASLMFFVOLPSNTTWLTKVNLVLPHTNLTLATQYLL--VDASGMHOL 180  
 116 PLMSHNLVHARL--WLHVPRSPGTLYLIRFCG--TTRCGSRFTLAHQTTSSGMHAL 171  
 DB 181 PLGPEAOACSGCHLTLELV-----LEGOVAOSSVILGAA--HRPFVARVAVG--GKH 231  
 172 TLPSGLNSEDSGVYKQLERPRPLDLNSTAAGLPRLLDLTAQOQRPFLKIRANEPGAG 231  
 QY 232 QIHRGIDCGGSRMCCROEFVDREIGMHDIIOPEGYAMNFCIGCPPLHAGMPCIA 291  
 232 RARRRTPCESEPTLCCRDHYVDQELGMRDITLOPEGYOLNCGGCPPLHAGSPGIA 291  
 DB 292 ASFTAVLNLKANTAACTGGSCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGC 351  
 292 ASFTAVLNLKANTAACTGGSCVPTARRPLSLIYDRDSNIYKTDIPDMVVEACGC 351  
 QY 352 S 352  
 DB 350 S 350

RESULT 7  
ID INHB\_BOVIN STANDARD: PRT: 408 AA.  
AC P42917:  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inhibin beta B chain precursor (Activin beta-B chain).  
GN INHB.  
OS Bos taurus (Bovine).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
OC Bovidae; Bovinae; Bos.  
CX NCBI\_TaxID=9913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Liver;  
RX MEDLINE=95112839; PubMed=7813465;  
RA Thompson D.A., Cronin C.N., Martin F.;  
RT "Genomic cloning and sequence analyses of the bovine alpha-, beta A-  
RT and beta B-inhibin/activin genes. Identification of transcription  
RT factor Ap-2-binding sites in the 5'-flanking regions by DNase I  
RT footprinting";  
RL Eur. J. Biochem. 226:751-764(1994).  
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
CC ACTIVINS.  
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC -----  
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CC or send an email to license@sib-sib.ch).  
CC -----  
DR EMBL: U16241; AAB60628.1; JOINED.  
DR EMBL: U16240; AAB60628.1; JOINED.  
DR HSSP: P18075; IBMF.  
DR InterPro: IPR002400; GF\_Cysknob.  
DR InterPro: IPR000381; Inhibin\_betaB.  
DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGFb\_N.  
DR Pfam: PF000019; TGF-beta\_1.  
DR Pfam: PF00688; TGF-beta\_propeptide\_1.  
DR PRINTS: PR00438; GF\_CYSKNOB.  
DR PRINTS: PR00671; INHIBINB.  
DR Prodom: PD000357; TGF-beta\_1.  
DR SMART: SM00204; TGFb\_1.  
DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
KW Growth factor; Hormone; Glycoprotein; Signal.  
FT SIGNAL 1 28  
FT PROPEP 29 293  
FT CHAIN 294 408  
FT DISULFID 297 305  
FT DISULFID 304 373  
FT DISULFID 333 405  
FT DISULFID 337 407  
FT DISULFID 372 372  
INTERCHAIN (BY SIMILARITY).

FT CARBOHD 94 94 N-LINKED (GLCNAC... ) (POTENTIAL).  
SO SEQUENCE 408 AA: 44897 MW: EF497DB30D2897DF CRC64:  
Query Match 32.7%; Score 605; DB 1; Length 408;  
Best local similarity 36.6%; Pred. No. 1,2e-47;  
Matches 145; Conservative 62; Mismatches 117; Indels 72; Gaps 15;  
QY 13 APTVATPRA-----GGQ---CPACGGPTLELESOREL-----LDDAKRSIL 52  
DB 29 SPTPEPLDPAAPPPPPPCAPGSDPTCTSCG-----FRPEELGRVDGDELEAVKRHL 84  
QY 53 DKHLTQPTPLRPYSRAALRTALQHLHGVPQALLDNR-----EQE 95  
DB 85 NRLQGRPNITHAVPKAMVTALRKLHA---GKVEDGAEVEIPLHGDHASPGADGGRV 141  
QY 96 CEISFAENGSLTINOTRIDFHFSSDRTAGDRE--VQASLMFFVOQPSNTTWL----- 148  
DB 142 SEIISFAETDGLASSVRVLPFTSNE--GNQLFVQASLMDYLKL---LPVLEKGR 195  
QY 149 -KVRVLYGLPIIN--TNLTATQYLLEVDASGMHQLPLGPEAOAASOGHLTLEVLGQV 205  
DB 196 RKVRKVVYGOEGPDDMAAVERKRDVLRKSGMHTFPTQLFSGEKRLSLDVQODS 255  
QY 206 AQSSTVL-----GGAHRPFVAVARYRG-GKHQIRRRGIDCGSRMCCROEFFVDFRE 258  
DB 256 CRELAIVVFVDFGESHRRPFVYVQARLGDSSRRIRKRGLECGRTNLCCROEFFDFRL 315  
QY 259 IGMHWMIOPBEGYANRFGICGCPPLHAGPGLAASHTAVNLKNTAAGTTCG--GSC 316  
DB 316 IGMHWMIAPGYGYNGYCEGSPAVLAGVGSASFHTAVNGYRMR---GLMGTVNSC 372  
QY 317 CVPTARRPLSLYYDRDSNIYKTDIPDMVVEAGCS 352  
DB 373 CIPKLSMSMLYDDEYNIYKRDYPMNIVECGCA 408  
RESULT 8  
ID INHB\_HUMAN STANDARD: PRT: 407 AA.  
AC P09529;  
DT 01-MAR-1989 (Rel. 10, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inhibin beta B chain precursor (Activin beta-B chain).  
GN INHB.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
CX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=90114200; PubMed=2575216;  
RA Mason A.J., Berkemeyer L.M., Schmeizel C.H., Schwall R.H.;  
RT "Activin B: precursor sequences, genomic structure and in vitro  
RT activities";  
RL Mol. Endocrinol. 3:1352-1358(1989).  
RN [2]  
RP SEQUENCE OF 22-407 FROM N.A.  
RX MEDLINE=89295443; PubMed=2739657;  
RA Feng Z.M., Bardin C.W., Chen C.L.;  
RT "Characterization and regulation of testicular inhibin beta-subunit  
RT mRNA";  
RL Mol. Endocrinol. 3:939-948(1989).  
RN [3]  
RP SEQUENCE OF 55-407 FROM N.A.  
RX MEDLINE=86186863; PubMed=3754442;  
RA Mason A.J., Miall H.D., Seeburg P.H.;  
RT "Structure of two human ovarian inhibins";  
RL Biochem. Biophys. Res. Commun. 135:957-964(1986).  
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION.

CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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CC EMBL; M31669; AAA59451.1; -  
 CC EMBL; M31668; AAA59451.1; JOINED.  
 CC EMBL; M31682; AAA59170.1; -  
 CC EMBL; M31437; AAA59169.1; -  
 CC PIR; C24248; C24248.  
 CC HSSP; P18075; 1BMP.  
 CC MIM; 147390; -  
 CC InterPro; IPR002400; GF\_cysknob.  
 CC InterPro; IPR000381; Inhibin\_betaB.  
 CC InterPro; IPR001839; TGF-beta.  
 CC InterPro; IPR001111; TGFb.N.  
 CC Pfam; PF00019; TGF-beta.1.  
 CC Pfam; PF00688; TGFb\_propeptide; 1.  
 CC PRINTS; PR00438; GFCYSKNOT.  
 CC PRINTS; PR00671; INHIBINB.  
 CC PRODOM; PD000357; TGF-beta; 1.  
 CC SMART; SM00204; TGFb.1.  
 CC PROSITE; PS00250; TGF\_beta.1; 1.  
 CC Growth factor; Hormone; Glycoprotein; Signal.  
 CC SIGNAL 1 28  
 CC PROPEP 29 292  
 CC CHAIN 293 407  
 CC DISULFID 296 407  
 CC DISULFID 303 372  
 CC DISULFID 332 404  
 CC DISULFID 336 406  
 CC DISULFID 371 371  
 CC CARBOHD 93 93  
 CC CONFLICT 47 47  
 CC SEQUENCE 407 AA; 45121 MW; 90316C8597BA6B4 CRC64;

Query Match 32.4%; Score 599.5; DB 1; Length 407;  
 Best Local Similarity 36.6%; Pred. No. 3.9e-47;  
 Matches 145; Conservative 60; Mismatches 118; Indels 73; Gaps 16;

QY 13 APTTVAAPRA-----GGO---CPACGGPPLLESQEL-----LDDAKRSILD 53  
 DB 29 SPPPTTPAPAPPPPPGSGSDTCTSCG---FRPELGRVDSDFEAVKRRHLS 84  
 QY 54 KLHLTQRPFLNRYSAALPTALQHLGVPQGALLEENR-----EORC 96  
 DB 85 RLOMRGPNLTTHAVPKAMATLKLHA--GKVEDGRVEIPHLIDGASPADDOEKRS 141  
 QY 97 EISFAETGLSTINOTRDLPHSSDRFAGRE--VOQASLMEFVQLPSNTWTWL----- 148  
 DB 142 EISFAETGLDGLASSRVLTFISNE--GNQNLFFVQASLMLYLT--LPVLEKGRSR 195  
 QY 149 KVRVLYL---GPHNTLTLATOLYLEVDASGWHOLPLCPREAOACSGCHLTLELVLEGOV 205  
 DB 196 KVRKVVYFQEGHGDWRNM--VEKRVDLKRSQWHFRPLTEALQALREKERRRLNDVQCD 254  
 QY 206 AOSVYL-----GGAHRRPVAAVRVYG-GKHQTHRGIDQGGSRMCCRFQFVDFRE 258

DB 255 COLAVPVVDEPDESHRRPVVVOAHLRGDSRRHRIRKKGLEDGDTNLCCHQOFIDPRL 314  
 QY 259 IGWHDWITQEGYAMNFCIGCPPLHAGMPGIAASFHTAVLNLKANTAGTTGG--GSC 316  
 DB 315 IGWHDWITAPTYGVCNCEGSCGPAYLAGVPGSASSFHTAVVQYBMR--GIMPQVNSC 371  
 QY 317 CVPARPRLSLTYDRDSNITYKTIDPMVVEACGCS 352  
 DB 372 CIPTKLSTMSMLYFDEYIVKRDVPMNIVECGCA 407

## RESULT 9

INHB\_CHICK STANDARD; PRT; 391 AA.  
 AC P27093; 073796;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta B chain precursor (activin beta-B chain).  
 GN INHB.  
 OS Gallus gallus (Chicken).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 CC NCBI\_TaxID=9031;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=follicle;  
 RA Klingner H., Halsechek-Wiener J., Mohlrad B.K., Kuchler K., Mohlrad F.;  
 RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=WHITE LECHORN; TISSUE=Ovary;  
 RA Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;  
 RL Submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE OF 311-381 FROM N.A.  
 RX MEDLINE=91029482; PubMed=2225063;  
 RA Mitrani E., Ziv T., Thomsen G., Shimon Y., Melton D.A., Brill A.;  
 RT "Activin can induce the formation of axial structures and is expressed  
 RT in the hypoblast of the chick."  
 RL Cell 63:495-501(1990).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOPHYSALIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC  
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DR InterPro: IPR002400; Gf\_cysknot.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA\_1; 1.  
 DR Growth factor; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1  
 FT PROPEP 26 276  
 FT CHAIN 277 391  
 FT DISULFID 280 288  
 FT DISULFID 287 356  
 FT DISULFID 316 388  
 FT DISULFID 320 390  
 FT DISULFID 355 355  
 FT CARBOHYD 77 77  
 FT CONFLICT 30 30  
 FT SEQUENCE 391 AA; 43608 MW; 060017BF3E7AF6C CRC64;

Query Match 32.3%; Score 598; DB 1; Length 391;  
 Best Local Similarity 34.8%; Pred. No. 5, 1e-47;  
 Matches 136; Conservative 69; Mismatches 138; Indels 48; Gaps 11;

QY 1 MSSLLAELLAPTVAPRAGQ-----CPACGGPTLESCORE-LLDLAKRSILDK 54  
 DB 10 LAAALLACGLLLGAAATPPRAGSSPDCTSCGFRPRPERPKVDDFLAVKRLILSR 69  
 QY 55 LHLTPRTLNRPYSRAALRTALOHLCVPGALLDNR-----EDQCE 97  
 DB 70 LQMRDRPNTTHAVPKAAMVATLAKLHA--GKVRDGRVETPSLDGASAPRAHDVSE 126  
 QY 98 IISFAETGLSTINQRLDHFSSDRTAGRE--VQASLMFVQ-----LPSNTTWLTKV 150  
 DB 127 IISFAETGLSTINQRLDHFSSDRTAGRE--VQASLMFVQ-----LPSNTTWLTKV 150  
 QY 151 RVLVAGPHNTNLTATQYLLEVDASGWHOLPLCEPAQACSGHLELVLEGVQACSSV 210  
 DB 184 KVFYFDDPTSNKWNVEKRVKDLKRSQMHFPMTEATQALFERGERRLNLDVQCEGEYS 243  
 QY 211 IL-----GGAHRPPVAVARVYG-GKHQIHRGIDCGGSRACQCFVVDREIGMAD 263  
 DB 244 VLPITVDGEEHREPLVYQARLADKHKIRKGLCCDGTNLCGQOQFYIDRLIGMND 303  
 QY 264 WIDPEGYAMNFCIGCCPLHAGMPGIAASFHTAVLNLKANTAGTTGG--GSCCVPFA 321  
 DB 304 WIAPSGYGVNCEGSCPAYLAGVPGSASFHTAVVNOYRMR---GLNGETVNSCCLPTK 360  
 QY 322 RRPSSLVYDRSNIVKVDIPMVYVACGCS 352  
 DB 361 LSTWMSLYFDDENYIVKRDVPMVIVECCGA 391

RESULT 10  
 ID IHHB\_PIG STANDARD; PRT; 349 AA.  
 AC P04088;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).  
 GN IHHB.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovarian follicular fluid;  
 RX MEDLINE=86092207; PubMed=2417121;  
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Deno N., Ying S.-Y.,

RA Guillemin R., Niall H., Seeburg P.H.;  
 RT \*Complementary DNA sequences of ovarian follicular fluid inhibin show  
 RT precursor structure and homology with transforming growth  
 RT factor-beta.";  
 RL Nature 318:659-663(1985).

RP SEQUENCE OF 235-249.

RA MEDLINE=92355604; Pubmed=1644823;

RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,  
 RT Arizumi T., Yashiro T., Sugino K., Tani K., Sugino H.;  
 RT Isolation and characterization of native activin B.";  
 RL J. Biol. Chem. 267:16385-16389(1992).

-1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.

INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 FUNCTIONS SUCH AS HYPOPHYSALIC AND PITUITARY HORMONE SECRETION,  
 GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 ACTIVINS.

-1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.

INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 INHIBIN B IS A DIMER OF ALPHA AND BETA-B.

ACTIVIN A IS A HOMODIMER OF BETA-A.  
 ACTIVIN B IS A HOMODIMER OF BETA-B.

ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.

-1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).

EMBL: X03267; CA927021.1; -

PIR: A01394; WPCGBB.

HSSP: P18075; IBBP.

InterPro: IPR001839; TGF-beta.

InterPro: IPR001111; TGF-beta.

Pfam: PF00019; TGF-beta; 1.

Pfam: PF00688; TGF-beta; 1.

ProDom: PD000357; TGF-beta; 1.

SMART: SM00204; TGF-beta; 1.

PROSITE: PS00250; TGF-BETA\_1; 1.

Growth factor; Hormone; Glycoprotein.

FT PROPEP 1 234  
 FT CHAIN 235 349  
 FT DISULFID 238 246  
 FT DISULFID 245 314  
 FT DISULFID 274 346  
 FT DISULFID 278 348  
 FT DISULFID 313 313  
 FT CARBOHYD 35 35  
 FT SEQUENCE 349 AA; 39354 MW; C571EA91ADA5DE77 CRC64;

Query Match 31.7%; Score 587; DB 1; Length 349;  
 Best Local Similarity 37.7%; Pred. No. 4, 5e-46;  
 Matches 129; Conservative 62; Mismatches 109; Indels 42; Gaps 9;

QY 44 LIDLAKSILDKLHTPRTLNRPYSRAALRTALOHLCVPGALLDNR----- 92  
 DB 17 LEAVKRILRLRQMRGNITTHAVPKAAMVATLAKLHA--GKVRDGRVETPSLDGAS 73  
 QY 93 -----EQCEIISFAETGLSTINQRLDHFSSDRTAGRE--VQASLMFVQ----- 139  
 DB 74 PGADGQERSEIISFAETGLSTINQRLDHFSSDRTAGRE--VQASLMFVQ----- 130  
 QY 140 LPSNTTWLTKVRLVLCGPHNTNLTATQYLLEVDASGWHOLPLCEPAQACSGHLELV 199

Db 131 LEKSGRRKRVKVFQEPFGHGRMDVVERKVDLKRSGWHTTLPLETEIAQLFEGEKRLNL 190  
 OY 200 VLEGQVASSVYL-----GGAHRRPFAARVAVG-GKHQIHRGIDCGGSRMCCROEF 252  
 Db 191 DVQDGGCEGLAVPVPVPGESHHPFVYVQARLDGSRIRKRGLECGRTLCRRQOF 250  
 OY 253 FVDFREIGWMDWITQPEGYAMNFCIGQCPPLHAGMGIASPHYAVNLKANTAACTTG 312  
 Db 251 FIDRLIGMSWILAPGTGYNGYCGSPAYLAGVGSASFHTAVVNOYRMR---GLNP 307  
 OY 313 G-GSCVPTARRPLSLTYDPSNVKRTDIDPMVEACGCS 352  
 Db 308 GTVNSCCIPTKLSTMSMLYFDEYNTVKRDVPMVIEEGCA 349

RESULT 11  
 ID INHA\_PIG STANDARD: PRT: 424 AA.  
 AC P03970:  
 DT 23-OCT-1986 (Rel. 02, Created)  
 DT 23-OCT-1986 (Rel. 02, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta A chain precursor (Activin beta-A chain).  
 GN INHBA.  
 OS Sus scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OC NCBI\_TaxID=9823;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Follicular fluid;  
 RX MEDLINE=86092207; PubMed=2417121;  
 RA Mason A.J., Hayflick J.S., Ling N., Esch F., Deno N., Ying S.-Y.,  
 RA Guillemin R., Nalil H., Seeburg P.H.;  
 RT \*Complementary DNA sequences of ovarian follicular fluid inhibin show  
 RT precursor structure and homology with transforming growth  
 RT factor-beta.\*;  
 RL Mature 318:659-663(1985).  
 RN [2]  
 RP SEQUENCE OF 309-323.  
 RC TISSUE-Follicular fluid;  
 RX MEDLINE=92355604; PubMed=1644823;  
 RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,  
 RA Arizumi T., Yashiro T., Sugino K., Tlatal K., Sugino H.;  
 RT Isolation and characterization of native activin B.\*;  
 RL J. Biol. Chem. 267:16385-16389(1992).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC or send an email to [license@1sb-sib.ch](mailto:license@1sb-sib.ch)).  
 CC EMBL: X03266; CAA27020.1;  
 DR PTR: A01393; WFPGBA.

DR HSSP: P18075; 1BMP.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR000491; Inhibin\_beta.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGFb-N.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR PRINTS: PR00438; GFCYSKNOR.  
 DR PRINTS: PR00670; INHIBINB.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor: Hormone; Glycoprotein; Signal.  
 KW SIGNAL: 1 20  
 FT PROPER 21 308  
 FT CHAIN 309 424  
 FT DISULFID 312 320  
 FT DISULFID 319 389  
 FT DISULFID 348 421  
 FT DISULFID 352 423  
 FT DISULFID 388 388  
 FT CARBOHYD 165 165  
 SQ SEQUENCE 424 AA; 47476 MW; 436BC62226FADF52 CRC64;  
 N-LINKED (GLCNAC...) (POTENTIAL).  
 Query Match 30.4%; Score 562; DB 1; Length 424;  
 Best Local Similarity 31.2%; Pred. No. 1,1e-43;  
 Matches 131; Conservative 69; Mismatches 142; Indels 78; Gaps 10;  
 OY 6 LIAFLLAFTVATVATPAG-----QCPACGPTL-ELSESORELLIDARKSLIDKHLT 58  
 Db 10 LASCWITVRSSTPSSGSHSAAPDCSCALATLPKDVPSQPEMVAVKHILMLHLK 69  
 OY 59 QRPRTNRPVSRALRTALQHLH-----GVPGALLDNRQECETISFAET 104  
 Db 70 KRPDVQPPPKALLAIAIKRLHYGVKGENGYELEDIGRAEENLEIEMQTSIITPAEA 129  
 OY 105 GLSTINOTRLDPIFSSDRTRAGDRE-VQASLMEFVQLPSNTWTWLRVVLVS----- 156  
 Db 130 GTA-----RKLTFEISKEGSDLSVERAETWLFVKPKANRTKVSIRLPQOORRPOG 184  
 OY 157 -----PHNDNLTLATQYLLVDASGWHQPLPDEAQ-----AAC 190  
 Db 185 SADAGEADEVDYCFPEEKSEVLISEKVDARKSTWHIFPVSSIORLDDQKSAIDIRAC 244  
 OY 191 SOGHLT-LLEVLDEGOVASSVILG-----AHRPFAARVAVGK--HQ 232  
 Db 245 EQCHEGASLVLLGKKKKKEEAEGRKRDGAGVDEKEQSHRFLMLARQSEEHHR 304  
 OY 233 IHRGIDCGGSRMCCROEFFVDFREIGWMDWITQPEGYAMNFCIGQCPPLHAGMGIASPH 292  
 Db 305 RRRRGLECDGKVNICKKQFFVSFKDIGMDWITAPSGYHANYEGECPSHACTGSSSL 364  
 OY 293 SEFTAVNLKANTAACTTGSGCVCPTARRPLSLTYDPSNVKRTDIDPMVEACGCS 352  
 Db 365 SFHSTVINYHRMGHSPANLKSCTVFKLPMSMLYTDGONIIKKDIOMIYIECCGS 424

RESULT 12  
 ID INHA\_RAT STANDARD: PRT: 424 AA.  
 AC P18331;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta A chain precursor (Activin beta-A chain).  
 GN INHBA.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91042598; PubMed=3153478;

RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.,  
 RT "Ret inhibin: molecular cloning of alpha- and beta-subunit  
 RL complementary deoxyribonucleic acids and expression in the ovary."  
 CC Mol. Endocrinol. 1:561-568(1987).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS:  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: M37482; AAA41436.1; -  
 CC PIR: B40056; B40056.  
 CC HSSP: P18075; 1BMP.  
 CC Interpro: IPR002400; CF\_cysknoc.  
 CC Interpro: IPR004491; Inhibin\_betaA.  
 CC Interpro: IPR001839; TGF-beta.  
 CC Interpro: IPR001111; TGF-beta.  
 CC Pfam: PF00019; TGF-beta; 1.  
 CC Pfam: PF00688; TGF-beta; 1.  
 CC PRINTS: PR00438; GFCYSKNOT.  
 CC PRINTS: PR00670; INHIBINB.  
 CC PRODOM: PD000357; TGF-beta; 1.  
 CC SMART: SM00204; TGF-beta; 1.  
 CC DR SMART: SM00204; TGF-beta; 1.  
 CC DR PROSITE: PS00250; TGF\_beta\_1; 1.  
 CC KM Growth factor; Hormone; Glycoprotein; Signal.  
 CC FT SIGNAL 1 20  
 CC FT PROPEP 21 308  
 CC FT CHAIN 309 424  
 CC FT DISULFID 312 320 INHIBIN BETA A CHAIN.  
 CC FT DISULFID 319 389 BY SIMILARITY.  
 CC FT DISULFID 348 421 BY SIMILARITY.  
 CC FT DISULFID 352 423 BY SIMILARITY.  
 CC FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).  
 CC FT CARBOHYD 165 165 N-LINKED (GLCNAC... ) (POTENTIAL).  
 CC SQ SEQUENCE 424 AA; 47406 MW; B2DAF7917FA50984 CRC64;  
 CC -----  
 CC Query Match 30.3%; Score 561; DB 1; Length 424;  
 CC Best Local Similarity 33.0%; Pred. No. 1.3e-43;  
 CC Matches 139; Conservative 66; Mismatches 136; Indels 80; Gaps 13;  
 CC -----  
 CC QY 6 LLAFLAATVATPRAGS-----OCPCAGPTLE-----SOELLDLAKRSILDKLH 57  
 CC DB 10 LLAASWITVRSPPTGSEHGAPPCSCALITLPKDGNSQPE-NVEAVKKHILNMLHL 68  
 CC QY 58 TORPTLNRPVSAALRTALQHLH-----GYPOGALDEDRQEEIISPAE 143  
 CC DB 69 KRPDVTQPVKPAALLNLRKLHGVKGVGEIIEEDDGRRAEMLEFOTSEITFAE 128  
 CC QY 104 TGLSTINTRLDHFSSDRTAGDRE-VQOASLMEFVQDPSTNTWLTKRV- 152  
 CC DB 129 SGTA-----RKLHFEIKESGSDLSVERAEVFLKVKARTRPKVTRILFOQCKH 183  
 CC QY 153 --LVLCGPHNTLVLT--ATQVYLE--VDA--SGWHOLPLGDEAQAACSGHITDELVAE 202

DB 184 GSLDMDEAEEMGLKGERSELLSEKVDARKSTWHIFVSSIORLLDQGSLLDVRIA 243  
 QY 203 QVQAQS-----VITG-----GAHRPF--VAARVVGGRH 231  
 DB 244 CEQCEGASGLVLLGKKKKKEVDGKKKSDGGLKEEKKQSRPFLMLARQSEDPH 303  
 QY 232 QIHRGIDCGGSRMCCROEFFVDFREIGMDWIIIOPEGYAMNFCIGGCPHIAQMPGIA 291  
 DB 304 RRRRGLECGGVKVICCKKQRFVFKDGMNDWIIAPSGHANICEGCPSHIAGTSSG 363  
 QY 292 ASHTAVLNLKANTAACTGCGCVPTARRPLSLLYDRDSNVKTDIPDMVVEACGC 351  
 DB 364 LSFHSTVINYHMRGHSFPANLKCVCVPTKLRFPMSTLYDDGQNIKKIDQMIVEECG 423  
 QY 352 S 352  
 DB 424 S 424  
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 CC RESULT 13  
 CC ID I\_HBA\_HORSE STANDARD: PRT: 426 AA.  
 CC AC P5102;  
 CC DT 01-OCT-1996 (Rel. 34, Created)  
 CC DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 CC DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 CC DE Inhibin beta A chain precursor (Activin beta-A chain).  
 CC GN INHBA.  
 CC OS Equus caballus (Horse).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 CC OX NCBI\_Taxid-9796;  
 CC RN [1]  
 CC RP TISSUE-Ovary;  
 CC RC MEDLINE-96031670; PubMed-7548399;  
 CC RX Yoshida S., Yamanouchi K., Hasegawa T., Ikeda A., Suzuki M.,  
 CC RA Chang K., Matsuyama S., Nishihara M., Takahashi M.,  
 CC RT "Molecular cloning of cDNA for equine ovarian inhibin/activin beta A  
 CC subunit".  
 CC RL J. Vet. Med. Sci. 57:469-473(1995).  
 CC -----  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL: D50326; BAA08862.1; -  
 CC HSSP: P18075; 1BMP.  
 CC Interpro: IPR002400; CF\_cysknoc.  
 CC Interpro: IPR004491; Inhibin\_betaA.  
 CC Interpro: IPR001839; TGF-beta.  
 CC Interpro: IPR001111; TGF-beta.  
 CC Pfam: PF00019; TGF-beta; 1.



DR Pfam: PF00688; TGF-beta; 1.  
 DR PRINTS: PR00670; INHIBINB.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-beta; 1.  
 DR Growth factor: Hormone; Glycoprotein; Signal.  
 KW SIGNAL: 1  
 FT PROPEP 21 310  
 FT CHAIN 311 426  
 FT DISULFID 314 322 INHIBIN BETA A CHAIN.  
 FT DISULFID 321 391 BY SIMILARITY.  
 FT DISULFID 350 423 BY SIMILARITY.  
 FT DISULFID 354 425 BY SIMILARITY.  
 FT DISULFID 390 390 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAc...) (POTENTIAL).  
 SQ SEQUENCE 426 AA; 47709 MW; E481060B368A77D CRC64;

Query Match 30.3%; Score 560; DB 1; Length 426;  
 Best Local Similarity 32.5%; Pred. No. 1.7e-43;  
 Matches 137; Conservative 67; Mismatches 138; Indels 80; Gaps 12;

OY 6 LLAFLLLAFTVATPRAGG-----QCPACGGPTL--ELBSQRELLDLAKRSILDKLHLT 58  
 DB 10 LLASWIIIVKSSPTGSEGHSAAPNCSCALATLPKDVPAQPEWVAVKHLLMLHLK 69  
 OY 59 QRPPLNRPVSRALRATLOHL-----GVPGALLDREDECEITSPAE 104  
 DB 70 KRDPVTPQPKAALLNAIKRLHVGKGVNGEYEDIDIGRAEMNELDETSITPAES 129  
 OY 105 GLISTINORLDFHSSDRFAGRE--VOQASIMFEVOLPSMTWTLYKRVLV-----G 156  
 DB 130 GTA-----RKLHFEISKEGSDLSYVERAEVWLFKVPKANKRRTSKYTIKLLQOQKHPOG 184  
 OY 157 PHNTLLTATQYLL-----VDA--SGMHOLPLGPEAOACSGHLLTLEYLE- 202  
 DB 165 SSDTRFEAEADLMERSBOLISEKVVADARKSWHLPVSSIQRLDQKSSIDRIAC 244  
 OY 203 ---GVQVSSVILG-----GA-----AHRPF--VAAVRVGGK 230  
 DB 245 DQCHETGASLVLLKKKKKEEGECKKKDGEAGAGVDEKESHRFLMLQAQSEDPH 304  
 OY 231 HQIHRGICQCGGSRMCRCREFVDRFELGMDHIIIOPEGYAMNFCIGOCPLHAGMFI 290  
 DB 305 HRRRRRGLECDGKVNICKKQKQFVSEKIDGMNDIIPSGYHANYCEBECSSHAGTSGS 364  
 OY 291 AASFHTAVLNLKANTAAAGTGGSCCVPTARRPLSLYDRDSNIVYTDIPDVAEAGC 350  
 DB 365 SLSEFHTVINOYLRCHNPPANLKSOCVPTKLRPMHMYDDGONIIKKIDIONMIVECG 424  
 OY 351 CS 352  
 DB 425 CS 426

RESULT 14  
 ID IIBA\_MOUSE STANDARD; PRT; 424 AA.  
 AC 004998;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta A chain precursor (Activin beta-A chain).  
 GN INHIB.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=93321614; PubMed=8330535;  
 RA Albano P.M., Groome N., Smith J.C.;  
 RT Activins are expressed in preimplantation mouse embryos and in ES

RT and EC cells and are regulated on their differentiation.\*;  
 RL Development 117:711-723(1993).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.  
 CC -1- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: X69619; CAA49325.1;  
 CC PIR: S31440; S31440.  
 DR HSSP: P18075; Inhba.  
 DR MCD: MGI:96570; Inhba.  
 DR InterPro: IPR002400; GF\_cyknod.  
 DR InterPro: IPR00491; Inhibin\_betaa.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR PRINTS: PR00670; INHIBINB.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR Growth factor: Hormone; Glycoprotein; Signal.  
 KW SIGNAL: 1  
 FT PROPEP 21 308  
 FT CHAIN 309 424  
 FT DISULFID 312 320 INHIBIN BETA A CHAIN.  
 FT DISULFID 319 389 BY SIMILARITY.  
 FT DISULFID 348 421 BY SIMILARITY.  
 FT DISULFID 352 423 BY SIMILARITY.  
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAc...) (POTENTIAL).  
 SQ SEQUENCE 424 AA; 47392 MW; 80C251B875A47213 CRC64;

Query Match 30.2%; Score 559; DB 1; Length 424;  
 Best Local Similarity 32.1%; Pred. No. 2.1e-43;  
 Matches 135; Conservative 71; Mismatches 135; Indels 80; Gaps 12;

OY 6 LLAFLLLAFTVATPRAGG-----QCPACGGPTL--ELBSQRELLDLAKRSILDKLHLT 57  
 DB 10 LLASWIIIVKSSPTGSEGHSAAPNCSCALATLPKDVPAQPEWVAVKHLLMLHLK 68  
 OY 58 TQRPPLNRPVSRALRATLOHL-----GVPGALLDREDECEITSPAE 103  
 DB 69 KRDPVTPQPKAALLNAIKRLHVGKGVNGEYEDIDIGRAEMNELDETSITPAES 128  
 OY 104 TGLSTINORLDFHSSDRFAGRE--VOQASIMFEVOLPSMTWTLYKRVLVGPH-- 158  
 DB 129 SGTA-----RKLHFEISKEGSDLSYVERAEVWLFKVPKANKRRTSKYTIKLLQOQKHPO 183  
 OY 159 -----NTNLTATQYLLVDA--SGMHOLPLGPEAOACSGHLLTLEYLE 202





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Db 130 GTA-----RKLHFEISKEGSDLSVERAEVWLFKVPKANRTRKVTIRLFQOQKHPOG 184
QY 159 -----NTNLTATOTYLEVDASGWHOLPIGPEAOAACSOGHLLLELYEG 203
Db 185 SLDTGEAEVEYGLKGERSELLSEKVDARKSTWHVFPYSSIORLLDOGKSSLDVRIAC 244
QY 204 QVAOSS-----VILG-----GA-----AHRPF--VAARVRVGK 230
Db 245 EQOESGASLYLLGKKKKKEEGEGKKGGEGGAGADEKEQSHRPFLLQARQSEDP 304
QY 231 HQIHRGIDCGGSRMCCROEFFVDREIGWHDWIIQPEGYAMNCTGOCPLHAGMPGI 290
Db 305 HRRRRGIECDGKVNICKKQFVFSKIDGMDWIIAPSGYHANYCEGECPSHIAGTSGS 364
QY 291 AASFHTAVNLKANTAGTGGSCVPTARRPLSLYYDRDSNIVKTDIPDMVVEACG 350
Db 365 SLSEHSTVINHYRMGRHSPANLKCSCVPTKLPMSTLYDDGONITIKKDIONMIVEECG 424
QY 351 CS 352
Db 425 CS 426

```

Search completed: October 12, 2002, 02:06:54  
 Job time : 15.5 secs

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OM protein - protein search, using sw model

Run on: October 11, 2002, 23:57:49 ; Search time 42 Seconds

(without alignments)  
1449.862 Million cell updates/sec

Title: US-09-684-383-2

Sequence: 1 MTSLLFLFLAFTTATP.....DSNIVKTDIPDNYVACGCS 352

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP\_ARCHAEA:\*  
2: SP\_BACTERIA:\*  
3: SP\_FUNGI:\*  
4: SP\_HUMAN:\*  
5: SP\_INVERTEBRATE:\*  
6: SP\_MAMMAL:\*  
7: SP\_MHC:\*  
8: SP\_ORNITHINE:\*  
9: SP\_PHAGE:\*  
10: SP\_PLANT:\*  
11: SP\_RODENT:\*  
12: SP\_VIRUS:\*  
13: SP\_VERTEBRATE:\*  
14: SP\_UNCLASSIFIED:\*  
15: SP\_VIRUS:\*  
16: SP\_BACTERIAP:\*  
17: SP\_ARCHAEP:\*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	688.5	37.2	367	13	Q91696 xenopus lae
2	649	35.1	350	11	Q91XH3 mus musculu
3	607.5	32.9	370	13	Q91350 xenopus lae
4	584.5	31.6	395	13	Q9PW66 anguilla ja
5	573.5	31.0	393	13	Q90261 brachydano
6	564	30.5	392	13	Q9PWB8 carassius a
7	554	30.0	426	4	Q9HBP0 homo sapien
8	547	29.6	413	13	Q98660 cynops pyr
9	533	28.8	424	13	Q98SP9 meleagris g
10	518	28.0	404	13	Q9PW65 carassius a
11	514	28.0	404	13	Q9PWB8 cynops pyr
12	354	19.1	119	6	Q9SKP1 allurus ful
13	353.5	19.1	119	13	Q42125 pagrus mejo
14	353	19.1	115	13	Q9DGP1 cyprinus ca
15	353	19.1	115	13	Q9DGP6 oryzias lat
16	353	19.1	119	6	Q95N79 alluropoda

17	353	19.1	119	6	Q95KP2 ursus malay
18	352	19.0	138	13	Q9W6T9 09d69 brachydano
19	347	18.8	115	13	Q9DGF9 09d69 cyprinus ca
20	347	18.0	115	13	Q9DGF7 09d67 oryzias lat
21	329	17.8	115	13	Q9DGF2 09d62 cyprinus ca
22	326	17.6	115	13	Q9DGF8 09d68 oryzias lat
23	323.5	17.5	376	13	Q98TB4 098t4 oreochromis
24	323	17.5	373	13	Q90ZD1 090zd1 oncorhynch
25	323	17.5	373	13	Q90W17 090w17 salmo salar
26	320	17.3	373	13	Q9D18 09d18 salmo salar
27	319.5	17.3	376	13	Q90WC9 090wc9 morone saxa
28	319.5	17.3	376	13	Q90WC8 090wc8 morone amer
29	317.5	17.2	104	13	Q98B61 098b61 cynops pyr
30	317	17.1	377	13	Q98TB3 098tb3 morone chry
31	312	16.9	373	13	Q90ZD2 090zd2 oncorhynch
32	311	16.8	373	13	Q98UB3 098ub3 salvelinus
33	309.5	16.7	376	13	Q90W06 090w06 umbrina cir
34	307	16.6	120	13	Q9W6T8 09w6t8 brachydano
35	306.5	16.6	102	13	Q90388 090388 carassius a
36	305	16.5	389	13	Q90Y10 090y10 ictalurus p
37	304.5	16.5	102	13	Q90389 090389 carassius a
38	296.5	16.0	385	13	Q90W05 090w05 sparus aur
39	292.5	15.8	102	13	Q9DET3 09det3 oncorhynch
40	281	15.2	586	5	Q9VCG9 09vcg9 drosophila
41	280	15.1	102	13	Q90390 090390 carassius a
42	277	15.0	373	5	Q91643 091643 drosophila
43	272	14.7	102	13	Q9DET1 09det1 oncorhynch
44	270	14.6	375	6	Q95N97 095n97 bos taurus
45	267	14.4	432	13	Q9PWF9 09pwf9 brachydano

## ALIGNMENTS

## RESULT 1

Q91696 PRELIMINARY; PRT; 367 AA.  
ID Q91696;  
AC Q91696;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ACTIVIN D PRECURSOR.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
OC Xenopodinae; Xenopus.  
OX NCBI\_TaxID=8335;  
RN [1]  
R1 SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RX MEDLINE=95275314; PubMed=7755637;  
RA Oda S., Nishimatsu S., Murakami K., Ueno N.;  
RT subunit: a dorsal mesoderm-inducing activity in Xenopus.\*;  
RL Biochem. Biophys. Res. Commun. 210:581-588(1995).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: D49543; BAA08494.1; -;  
DR HSSP: P12643; BMP.  
DR InterPro: IPR002400; GF\_cyskn0t.  
DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGFb.N.  
DR Pfam: PR00019; TGF-beta; 1.  
DR Pfam: PF00688; TGFb\_propeptide; 1.  
DR PRINTS: PR00438; GFCYSKN0T.  
DR PRODOM: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGFB; 1.  
DR PROSITE: PS00250; TGF-BETA; 1.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 253  
FT CHAIN 254 367  
FT SEQUENCE 367 AA; 41729 MW; C7E6334BD606FA04 CRC64;  
Query Match 37.2%, Score 688.5; DB 13; Length 367;

Best Local Similarity 40.4%; Pred. No. 4,5e-58;  
Matches 147; Conservative 65; Mismatches 125; Indels 27; Gaps 8;

OY 5 LLLALLAPTTVATPRAGGCPACGPTLELESORELLDLAKRSILDKLHTORPTLN 64  
DB 15 LLLALLAPTTVATPRAGGCPACGPTLELESORELLDLAKRSILDKLHTORPTLN 66  
OY 65 RVSAAALPTALOHILH-GVPOGALL-----EDNRECEIISPAETGISTINO 111  
DB 67 HEVPGAANALRLRLNPRMEGLEGSNSMDSNTENTDDQOSEIISPAETEXTENS 126  
OY 112 TRLDHFSSDRTACDREVOASLMPFVQLPNTTWLKVRLVLPHPNTNLATQVYLE 171  
DB 127 ITLNFQFTDKRO-SAHVLOAHLMLEFKANRTSOQNETIRLYQVAVSRILISEKLE 185  
OY 172 VDASGWHOLPLGPEAOACSGHLELVLEGOVASSVILGCA--AHPFAARVRVG 229  
DB 186 PRWTGOMFSLKSMLOTFPGGKSLQLLELNCOCQDPVLANPNSHQPLVVAQAKYHE 245  
OY 230 K-HOHRGICIDCGSRMCCROEFVDFREITGHWDMITIQEGYAMNFCIGCPLHAGMP 288  
DB 246 QSHNATKSLNCDONSILCCRKYDVDFKIDGWNMIKPEGQINCYCMGLCPHIIAGAP 305  
OY 289 GIASFHTAVLNLKANTAGTGGSCCVPTARPLSLIYDPDSNIVKTDIDPMVVEA 348  
DB 306 GMAASFHTVLMILKANNI--GTAVNSCCVPTARRPLSLMLYFDNRNNVLTADIADIVEA 363  
OY 349 CGCS 352  
DB 364 CGCS 367

## RESULT 2

OY1XH3 PRELIMINARY: PRT: 350 AA.  
AC G91350  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE INHIBIN BETA E.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER.  
RA Strausberg R.;  
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: BC010404; AAH10404.1;  
SQ SEQUENCE 350 AA; 39002 MW; 987EABAFAC389FA CRC64;

Query Match 35.1%; Score 649; DB 11; Length 350;  
Best Local Similarity 42.4%; Pred. No. 2.7e-54;  
Matches 153; Conservative 58; Mismatches 118; Indels 32; Gaps 14;

OY 6 LLLALLAPTTVATPRAGGCPACGPTLELESORELLDLAKRSILDKLHTORPTLN 65  
DB 8 LLLALLAPTTVATPRAGGCPACGPTLELESORELLDLAKRSILDKLHTORPTLN 65  
OY 66 PVSRAALRTALOHILHGVPOGALLLEDRRECEIISFA---ETGLSTINOTRDPHFSSDR 122  
DB 66 PVSRAALRTALOHILHGVPOGALLLEDRRECEIISFA---ETGLSTINOTRDPHFSSDR 122  
OY 123 TAGDREVOASLMPFVQLPNTTWLKVRLVLPHPNTNLATQVYLE--VASGWHOL 180  
DB 116 PLMSHHLVHARL--WLVHPSPFGTLVLRIFRCG--TTRCRGRPTFLAEHQTSSGHAL 171  
OY 181 PLGPEAOACSGHLELVLEGOVASS-----VILGCA--HHPFAARVRVG--GKH 231  
DB 172 TLPSGSLRSEDSGVYKQLLEFRRLDNLSTAGLPRLLDPTAQOQRFLEKIRANEPGAG 231  
OY 232 QIHRGIDCGSRMCCROEFVDFREITGHWDMITIQEGYAMNFCIGCPLHAGPGLA 291

DB 232 RARRTPCEPPTLCRRDHVDFQELGWRDMIIQPEGLVLYCSGQCPHLAGSPGIA 291  
OY 292 ASFTAVNLKANTAGTGGSCCVPTARPLSLIYDRDSNIYKTDIDPMVVEACGC 351  
DB 292 ASFTAVNLKANTAGTGGSCCVPTARPLSLIYDRDSNIYKTDIDPMVVEACGC 349  
OY 352 S 352  
DB 350 S 350

## RESULT 3

OY1350 PRELIMINARY: PRT: 370 AA.  
AC G91350  
DT 01-NOV-1996 (Tremblrel. 01, Created)  
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE ACTIVIN BETA B SUBUNIT.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=93273083; PubMed=8500654;  
RA Dohrmann C.E., Hemmati-Briavolou A., Thomsen G.H., Fields A.,  
RA Woolf T.M., Melton D.A.;  
RT \*Expression of activin mRNA during early development in Xenopus  
RT laevis.\*;  
RL Dev. Biol. 157:474-483(1993).  
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: S61773; AAB26863.1;  
DR HSSP: P18075; 1BP.  
DR InterPro: IPR002400; GE\_cysknob.  
DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGF-beta.  
DR Pfam: PF00019; TGF-beta; 1.  
DR Pfam: PF00688; TGF-beta; 1.  
DR PRINTS: PR00438; GFCYSKNOB.  
DR Prodom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.  
DR PROSITE: PS00250; TGF-BETA; 1.  
KW Glycoprotein.  
SQ SEQUENCE 370 AA; 41679 MW; AD21502AC45F1DE9 CRC64;

Query Match 32.9%; Score 607.5; DB 13; Length 370;  
Best Local Similarity 36.6%; Pred. No. 3e-50;  
Matches 140; Conservative 70; Mismatches 122; Indels 51; Gaps 14;

OY 5 LLLALLAPTTVATPRAGGCPACGPTLELESORELLDLAKRSILDKLHTORPTLN 62  
DB 4 LLLALLAPTTVATPRAGGCPACGPTLELESORELLDLAKRSILDKLHTORPTLN 57  
OY 63 LNRPSRAALRTALOHILHGVPOGALLLEDRRECEIISFAET 104  
DB 58 LNRPSRAALRTALOHILHGVPOGALLLEDRRECEIISFAET 114  
OY 105 GLSTINOTRDPHFSSDRTRGDR--VOQASLMPFVQLPNTTWLKVRLVLPHPN 159  
DB 115 DDVTASRVLSEFTIANB--GNQMLFVQSLMLYLKLPVWDSRRIRIKVHFODARN 171  
OY 160 TNLATQVYLEVDASGWHOLPLGPEAOACSG--HLELVLEGOVASSVY-----L 212  
DB 172 PDKMNVKVKVDIRSGWHPLPTEALQSLREGEERLNLVEQDG--CGEYSVLPVYVDP 230  
OY 213 GGAHRPFVAARVRVG--GKHQIHRGIDCGSRMCCROEFVDFREITGHWDMITIQEGY 271  
DB 231 GESHHPFLVHARLADNKRIRKRGLECDGHTLCCROQYIDFRLLGMDWITAPAGY 290  
OY 272 ANNFCIGCPLHAGPGLAASFTAVNLKANTAGTGG--GSCCVPTARRPLSLI 329

DB 291 YGNCEGSCPAVLAVGPGSASFHTAVVNOYRMR---GLNPGTVNSCCIPFLKSTMSMLY 347  
 OY 330 YDRDSNIVKTDIPDMVEACGS 352  
 DB 348 FDEYNIVKRDVPMNIVECGCA 370

## RESULT 4

09PMG6 PRELIMINARY: PRT: 395 AA.

AC 09PMG6; PRELIMINARY: PRT: 395 AA.  
 DT 01-MAY-2000 (TREMblrel. 13, Created)  
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE ACTVYN B.  
 OS Anguilla japonica (Japanese eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
 OC Anguillidae; Anguilla.  
 OX NCBI\_Taxid=7937;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Mura T., Mura C., Eto Y., Nagahama Y.,  
 RT "Activin B gene is required for the initiation of spermatogenesis in  
 the Japanese eel, Anguilla japonica";  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL; AB025356; BAA83804.1; -.  
 DR HSP; P12643; 3BP.  
 DR InterPro: IPR00381; Inhibin\_beta.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF\_beta.  
 DR Pfam; PF00019; TGF\_beta.1.  
 DR Pfam; PF00688; TGF\_beta\_propeptide.1.  
 DR PRINTS; PRO0672; INHIBINB.  
 DR PRODOM; PD000357; TGF\_beta.1.  
 DR SMART; SM00204; TGF\_beta.1.  
 DR PROSITE; PS00250; TGF\_BETA.1.  
 KW Glycoprotein.  
 SQ SEQUENCE 395 AA: 43889 MW; FA56D62D18509A3 CRC64;

Query Match 31.6%; Score 584.5; DB 13; Length 395;  
 Best Local Similarity 35.2%; Pred. No. 5.4e-48;  
 Matches 134; Conservative 67; Mismatches 131; Indels 49; Gaps 12;

OY 13 APTVATPRAGGCGCPGLELESOREL-LDLAKRSILDKLHILQRTPLNPRVRAA 71  
 DB 23 APTETQVVSODTCASCGGOPEESGRMDIDLEAVKRHLNRLQKREKRNITPIKAA 82  
 OY 72 LRTALOHLGCVQALGLEDNR-----EOECETISFAETGLSTINOTL 114  
 DB 83 MTAALAKLHA---GKVRGREGVEIPNLDGHATYNNEXQETSETISAEIS-DELTSKS 137  
 OY 115 DEHF--SSDTAGDREVOQASL-MFEVQLP-----SNTTWLKYRVLYLGPHTNLTLA- 165  
 DB 138 SHFLILNSGCONLYLSQASIMLYFLRLPSASEKSRKVTYKYVQGTGAAMAAAAAAG 197  
 OY 166 -----TOYLLVDASGWHOLPLGPEAOAASQGHLLTLELVLEGOVAOSSYL-----GG 214  
 DB 198 GRMGLVEKREVELKRSQMTFPLEPVGVEFERGDRDLDVRCGCEAAAVLPVLVDPGD 257  
 OY 215 AAHRPVAARVRV-GKHQIHARGIDCGSGRMCCROEFVDFREIWMHDIIDPEGMA 273  
 DB 258 ESHRPLVVOARLADSKHRIKRGLECDGTGGLCCROOFTIDFLRMNDWITAPSGIFG 317  
 OY 274 NFICGCPHIAAGMPCIAASFHTAVLNLKANTAAGTTG--GSCCVPTARPLSLLYD 331  
 DB 318 NCEGSCPAVMACVPSSASSFHTAVVNOYRMR---GMSPGSMSCCIPFLKSTMSMLYFD 374

OY 332 RDSNIVKTDIPDMVEACGS 352  
 DB 375 DEYNIVKRDVPMNIVECGCA 395

## RESULT 5

090261 PRELIMINARY: PRT: 393 AA.

AC 090261; PRELIMINARY: PRT: 393 AA.  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE ACTVYN B.  
 OS Brachydanio rerio (Zebrafish) (Zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Danio.  
 OX NCBI\_Taxid=7955;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-95011555; PubMed-7926744;  
 RA Wiltbrodt J., Frederic R.M.,  
 RT "Disruption at mesoderm and axis formation in fish by ectopic  
 expression of activin variants: the role of maternal activin";  
 RL Genes Dev. 8:1448-1462(1994).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL; X76051; CAA53636.1; -.  
 DR HSP; P12643; 3BP.  
 DR ZFIN; ZDB-GENE-990415-2; Inhb.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001839; TGF\_beta.  
 DR InterPro: IPR001111; TGF\_beta.  
 DR Pfam; PF00019; TGF\_beta.1.  
 DR Pfam; PF00688; TGF\_beta\_propeptide.1.  
 DR PRINTS; PRO0438; GF\_CYSKNOT.  
 DR PRODOM; PD000357; TGF\_beta.1.  
 DR SMART; SM00204; TGF\_beta.1.  
 DR PROSITE; PS00250; TGF\_BETA.1.  
 KW Glycoprotein.  
 SQ SEQUENCE 393 AA: 43830 MW; FA769C4D9BE4D252 CRC64;

Query Match 31.0%; Score 573.5; DB 13; Length 393;  
 Best Local Similarity 34.3%; Pred. No. 6.2e-47;  
 Matches 134; Conservative 80; Mismatches 128; Indels 49; Gaps 14;

OY 1 MTSSLLAFLLAPTVATPRAG--GCGPACGPTLELESOREL-LDLAKRSILDKLH 56  
 DB 13 LSVTCLMACLLSVQSSLSGAEFGSQESQVCGILGHQEDSGRMDIDLEAVKRHLNRLQ 72  
 OY 57 LTQRTPLNPRVRAALRTALOHILGCVQALGLEDNR-----EOECETIS 100  
 DB 73 MREKRNITPIKAAVNTALAKLHA---GKVRGREGVEIPNLDGHANNEVQETSETIS 129  
 OY 101 FAETGLSTINOTRLDHFSSDRTAGRE--VOQASL-MFEVQLPSNTTWLKYRVLYL-- 155  
 DB 130 FASDDVTFKSSSLYFLINE---GNQNLVLDANLMLYKRLPGLTEKLLBAKVTVRYH 186  
 OY 156 -----GRHNTNLTAIOYLLEVDASGWHOLPLGPEAOAASQGHLLTLELVLEGOVAOSSVI 211  
 DB 187 SVEPGQNVHWM-MEKREVLKRSQMTFPLEPVGVEFERGDRDLDVRCGCEAAAV 245  
 OY 212 L-----GAARHPVAAVRV-RVCGKHQIHARGIDCGSG-RMCCROEFVDFREIWMH 263  
 DB 246 LPTLVDPSPSHRPLVVOARQADGKHRIKRGLECDGNGGNGCRQOFTIDFLRMND 305  
 OY 264 WIIPEGVAMNCCIGCPHIAAGMPCIAASFHTAVLNLKANTAAGTTG--GSCCVPTA 321  
 DB 306 WIIAPAGYGNVCEGSCPAVMACVPSSASSFHTAVVNOYRMR---GMSPGSMSCCIP 362  
 OY 322 RRLSLLYDRDSNIVKTDIPDMVEACGS 352  
 DB 363 LSTMSMLYFDDEYNIVKRDVPMNIVECGCA 393

## RESULT 6

OPMR8 PRELIMINARY; PRT; 392 AA.

AC 09PMR8; 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE ACTININ BETA B SUBUNIT PRECURSOR.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi; Cypriniformes; Cyprinidae; Carassius.

NCBI\_Taxid:7957;

RM (1)

RP SEQUENCE FROM N.A.

RC TISSUE-Ovary;

RX MEDLINE-97424746; Pubmed-9278859;

RA Ge W., Mura T., Kobayashi H., Peter R.E., Nagahama Y.;

RT "Cloning of cDNA for goldfish actinin beta B subunit, and the expression of its mRNA in gonadal and non-gonadal tissues."

RL J. Mol. Endocrinol. 19:37-45(1997).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF004669; AAB61468.1; -

DR HSSP: P12643; 3BMP.

DR InterPro: IPR000381; Inhibin\_betaB.

DR InterPro: IPR001318; Inhibin\_betaC.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGF-beta.

DR Pfam: PF00019; TGF-beta; 1.

DR Pfam: PF00688; TGF-beta; 1.

DR PRINTS: PR00671; INHIBINB.

DR PRINTS: PR00672; INHIBINB.

DR PRODOM: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

KW Glycoprotein; Signal.

FT CHAIN 1 23 POTENTIAL.

FT SIGNAL 1 23 ACTININ BETA B SUBUNIT.

SO SEQUENCE 392 AA; 43853 MW; 73AAAEIC0824508 CRC64;

Query Match 30.5%; Score 564; DB 13; Length 392;

Best Local Similarity 34.1%; Pred. No. 5.1e-46;

Matches 133; Conservative 79; Mismatches 130; Indels 48; Gaps 14;

QY 1 MTSLLLAPTLAPTTVA--TPRAGGCGPACG-GPTLEESORELLDLAKSLDKLHL 57

DB 13 LSVTCIAMCILSYOCISGACTVSOESOCASGCLGHPDQSGRMDTDFLEAVKRHLNRLQW 72

QY 58 TORPLNRPVSRALRTALQHLHGVPQALLDNR-----EOCEIISF 101

DB 73 RRPNTNTHIPKAAVMTALRKLHA---GKVRDORVELPNDGNAHNEVQDETSEIISF 129

QY 102 AETGLSTINOTRLDFHSSSDRTAGDRE--VOQASL-MFEVOLPS-----NTFWTLKRVV 152

DB 130 AESDVTTPSKSLYFLISNE---GQNMLYVLQANLMLYFKLLPGTQEKGLRKKVVRVRS 186

QY 153 LVLGPHNTLTLATQYLLEVDASGMHQLPLGPREQAACSGHLLLELVLEGOVAOSVTL 212

DB 187 YEPGQGNVHPRM-MEKRVLEKSGMHTFPVSEAVREMLAKGRRODLDIHGECCEANVLT 245

QY 213 -----GGAHRPFVAVAR-RVGGKHQIHRRGIDCQSG-SRMCCROEFVDFGMDW 264

DB 246 PTLVPSDPSHPRLLVVAQQAADSKHRIKRGLECDGTNGCLCRQOYIDFRLIGMDW 305

QY 265 IIPRGYANFICIGCPPLIAGMPGIAASFHTAVNLKANTAGTTGG--GSCCVPTAR 322

DB 306 IIPAGYGNVCEGSCGPAYMACVGSASSPHTAVNVQYRMR---GIPGSVNSCIPITKL 362

QY 323 RPLSLLYVDRDSNIYKTDIPDMVVEACGCS 352

DB 363 STMSMLYFDDEYNIYKRDVPMIIECGCA 392

## RESULT 7

OGHBP0 PRELIMINARY; PRT; 426 AA.

AC 09HBP0; 01-MAR-2001 (Tremblrel. 16, Created)

DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE HYPOTHEICAL 47.5 KDA PROTEIN.

OS Homo sapiens (Human)

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

NCBI\_Taxid:9606;

RM (1)

RP SEQUENCE FROM N.A.

RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,

RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,

RA Yu J., Han L.H.;

RT "Novel Human cDNA clones with function of inhibiting cancer cell growth."

RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF218018; AAG17260.1; -

DR HSSP: P18075; 1BMP.

DR InterPro: IPR002405; Inhibin\_alpha.

DR InterPro: IPR000491; Inhibin\_betaA.

DR InterPro: IPR001318; Inhibin\_betaC.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGF-beta.

DR Pfam: PF00019; TGF-beta; 1.

DR Pfam: PF00688; TGF-beta; 1.

DR PRINTS: PR00669; INHIBINA.

DR PRINTS: PR00670; INHIBINB.

DR PRINTS: PR00672; INHIBINB.

DR PRODOM: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

KW Glycoprotein; Hypothetical protein.

SO SEQUENCE 426 AA; 47454 MW; 339276317BD5B408 CRC64;

Query Match 30.0%; Score 554; DB 4; Length 426;

Best Local Similarity 31.5%; Pred. No. 5.3e-45;

Matches 133; Conservative 74; Mismatches 135; Indels 80; Gaps 12;

QY 6 LLAPELLAPTVATPRAGG-----OCPACGPTL--ELSESORELLDLAKSLDKLHL 58

DB 10 LLAQWIIIVRSPPRGSEGHSAAPDCPSALALPKDVPNSQPEMVAVKHILNMLHLK 69

QY 59 QRPLNRPVSRALRTALQHLH-----GVPQALLDNRDECEIISFAET 104

DB 70 KRPDVQVPRKALNLRKLHVGKGVNGYVEIEDDGRRAEMNELDQTSIIITAES 129

QY 105 GLSTINOTRLDFHSSSDRTAGDRE--VOQASL-MFEVOLP--SNTFWT-LKVVVLVLP-- 158

DB 130 GTA-----RKLHFEISKEGSLSYVERAEVMLFKVPANRRTKYITILPQOQKHPQG 184

QY 159 -----NTNLTATQYLLEVDASGMHQLPLGPREQAACSGHLLLELVLEG 203

DB 185 SLDTGEAEAEVGLKGERSEILLSEKVVDAKSTWHEFPVSSSIRLLDQKSSLDVRIAC 244

QY 204 QVQSS-----YILG-----GA-----AHRPF--VAARVVGK 230

DB 245 EOCESASLVLKCKKKKEEGEGCKKGGGAGADEKEQSHRPLMLQAROSBDHP 304

QY 231 HQIHRGIDCGGSRMCCROEFVDFREIGMDWIIIPRGYANFICIGCPPLIAGMPG 290

DB 305 HRRRRGLECGKKNICKCKQFPYFSKIDGMDWIIIPRGYANFICIGCPPLIAGMPG 364

QY 291 AASFHTAVNLKANTAGTTGGGSCVPTARRPLSLLYVDRDSNIYKTDIPDMVVEACG 350

DB 365 SLSTHSYVINYRMGRGHPFANLASCVCPTKLRPMKSMILYYDQGNLIKIDQMIYEECG 424



RESULT	11
ENTRY	S31440
TITLE	Inhibin beta-A chain - mouse
ALTERNATE_NAMES	activin A; mesoderm-inducing factor WEHI-MF
ORGANISM	Formal_name Mus musculus #common_name house mouse
DATE	13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change

ACCESSIONS S31440; A60087  
 REFERENCE S31439  
 #authors Albano, P.M.  
 #submission submitted to the EMBL Data Library, November 1992  
 #accession S31440  
 #status preliminary  
 #molecule-type mRNA  
 #residues 1-424 ##label ALB  
 #cross-references EMBL.X69619  
 #reviewed X60087

REFERENCE	above,
#authors	Albano, R.M.; Godsave, S.F.; Huylebroeck, D.; Van Nimmen, K. Isaacs, H.V.; Slack, J.M.W.; Smith, J.C.
#journal	Development (1990) 110:435-443
#title	A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia cells is activin A.
#cross-references	NUID:92155098
#accession	A60087
#molecule_type	protein
#residues	309-311, 'X', 313-318, 'XX', 321-325 ##label AL2
CLASSIFICATION	#superfamily Inhibin
SUMMARY	#length 424 #molecular_weight 47392 #checksum 2136

	Query Match	21.3%	Score 543	DB 6	Length 424:
	Best Local Similarity	47.5%	Pred. No. 1,138-76		
Matches	66;	Conservative	30;	Mismatches 41;	Indels 2; Gaps 2;
Db	286 shrpflmlqasqdshprirrrrglcedgkvyalckokqfivsfkdigwndwllapsgyha	345			
Oy	216 AHRFVAARVAVRGKH-QIHRR-GIDCGGSRWCCRQEFYDERRIGTGMWIIOPEGYAM	273			
Db	346 nyccegcshlaigtgszslstnatvlnhyrmgmhsfnalkscvcyytlrlpmamlpyddg	405			
Oy	274 NFGICGCLHLAGMGFIASFTFAVLNLTAKNTAACTGGSCCVLPARRPUSLITDRD	333			

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Db      406 qnllkxdlqnmIveecgs 424
      11:1 1 1 :1:1 1111
QY     334 SNIVKIDIPDMVEACGS 352

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RESULT	12
ENTRY	S50898
TITLE	Inhibin beta A chain precursor - bovine
ALTERNATE_NAMES	activin; mesoderm inducing factor
ORGANISM	Bos primigenius taurus #common_name cattle
DATE	01-Aug-1995 #sequence_revision 01-Sep-1995 #text_change

SEQUENCE COMPARISON

ACCESSIONS	25-MAY-1996
REFERENCE	S50898; B25732; A60960; B61548
Authors	S50897
#Journal	Thompson, D.A.; Cronin, C.N.; Martin, F.
#Title	Eur. J. Biochem. (1994) 226:751-764
	Genomic cloning and sequence analyses of

beta(A)- and beta(B)-immunoglobulin genes. Identification of transcription factor AP-2-binding sites in the 5'-flanking regions by DNase I footprinting.

SEQUENCE COMPARISON A

#authors  
 Forstae, R.G.; Rung, J.M.; Brown, R.W.; McInerney, B.V.;  
 Cobon, G.S.; Gregson, R.P.; Robertson, D.M.; Morgan, F.J.;  
 Hearn, M.T.W.; Findlay, J.K.; Wettenhall, R.E.H.; Burger,  
 H.G.; De Kretser, D.M.  
 #journal  
 Proc. Natl. Acad. Sci. U.S.A. (1986) 83:3091-3095  
 #title  
 Cloning and sequence analysis of cDNA species coding for the  
 two subunits of inhibin from bovine follicular fluid.  
 #cross-references  
 #accession  
 825732

##molecule\_type mRNA  
##residues 258-425 ##label FOR  
##note part of this sequence, including the amino end of the  
mature protein, was confirmed by protein sequencing

REFERENCE  
#authors AG0960  
Chertov, O. Y.; Krasnosel'skii, A. L.; Bogdanov, M. E.;  
Hoperskaya, O. A.  
Blomed. Sci. (1990) 1:499-506  
Mesoderm-inducing factor from bovine amniotic fluid:  
purification and N-terminal amino acid sequence  
determination.

#accession	#molecule-type	#residues	#journal	#title	#accession	#molecule-type	#residues
A00900	protein	310-312, 'X', 314-319, 'XX', 322-328, 'P'		**label CHE			
A61548							
Fukuda, M.; Miyamoto, K.; Hasegawa, Y.; Nomura, M.; Igarashi, M.; Kangawa, K.; Matsuo, H.							
Mol. Cell. Endocrinol. (1986) 44:55-60							
Isolation of bovine follicular fluid inhibin of about 32 kDa							
B61548							
	protein	310-313		**label FUK			

GENETICS	130/1
#introns	#superfamily inhibit
CLASSIFICATION	disulfide bond; glycoprotein; gonad; heterodimer; homodimer;
KEYWORDS	hormone
FEATURE	
1-28	#domain signal sequence #status predicted #label sig\
29-109	#domain propeptide #status predicted #label pro\
310-425	#product beta1 inhibit/activin #status experimental
	#label MAT\
	#binding_site carbohydrate (Asn) (covalent) #status
165	predicted
SUMMARY	#length 425 #molecular-weight 47521 #checksum 898

Query Match	21.30;	Score 543;	DB 6;	Length 425;
Best Local Similarity	47.50;	Pred. No. 1.13e-76;		
Matches	66;	Conservative	30;	Mismatches 41;
			Indels	2;
			Gaps	2

```

Db 287 shupclmqarsedphurrirrgjcedgkvniceckkfvtgskldqwndwllapsyha 346
    : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Oy 216 AHRPEVARVRVGRKH-QIHR-GLDCOGSGMSRCROEFDFREIGMDWDIIOPETIAM 273

```

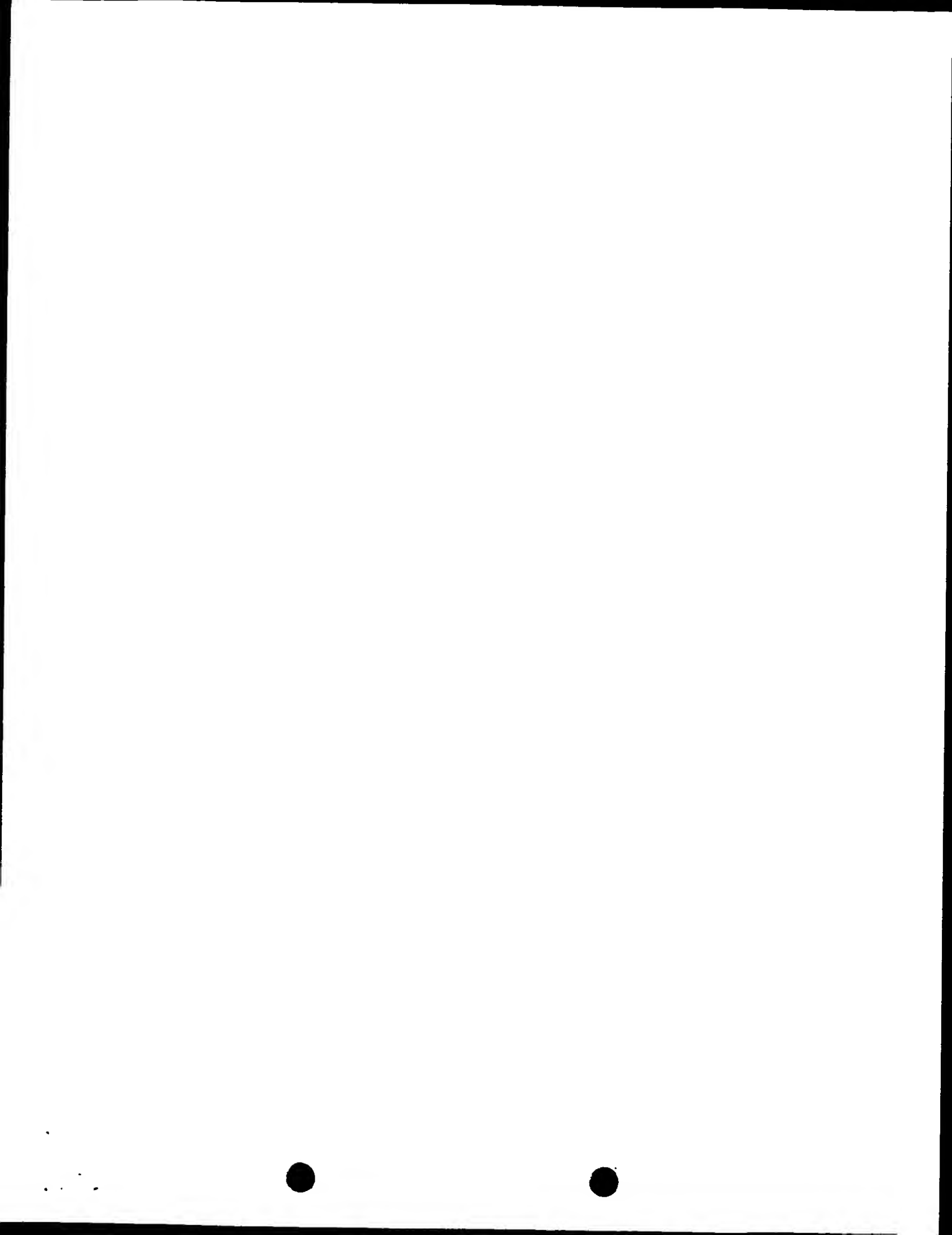
[illegible]

Db 407 gnllkkdlqnmLveecgcs 425  
||:| |:|:| | ||  
J/qy 334 snivktdlpmvEAcGCS 352

```

RESULT      13
ENTRY
TITLE
ALTERNATE_NAMES
SYNOPSIS
ORGANISM
B34248      *type complete
            inhibin beta-A chain precursor - human
            activin A; activin AB chain A; erythroid differentiation
            factor; megakaryocyte differentiation active protein
            *formal_name Homo sapiens *common_name man
            21-May-1988 *sequence_revision 21-May-1988 *text_change
            06-Sep-1996

```



OY 351 CS 352  
DB 425 CS 426

## RESULT 8

ID 098860 PRELIMINARY: PRT: 413 AA.

AC 098860; TREMBLrel. 02, Created)  
DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)  
DT 01-FEB-1997 (TREMBLrel. 19, Last annotation update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE ACTIVIN BETA-A SUBUNIT.  
OS Cynops pyrrhogaster (Japanese common newt).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Caudata; Salamandridae; Cynops.  
OX NCBI\_TaxID=8330;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=TESTIS.  
RX MEDLINE=96295508; PubMed=8702409;  
RA Yamamoto T., Nakayama Y., Abe S.;  
RT "Expression of activin beta subunit genes in sertoli cells of newt  
testis."  
RL Blochem. Biophys. Res. Commun. 224:451-456(1996).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: D84516; BAI12693.1; -.  
DR HSSP: P18075; 1BMP.  
DR InterPro: IPR002400; GF\_cysknoc.  
DR InterPro: IPR000491; Inhibin\_betaa.  
DR InterPro: IPR001839; TGF\_beta.  
DR InterPro: IPR001111; TGF\_beta.  
DR Pfam: PR000688; TGF\_beta; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR PRINTS: PR00670; INHIBINB.  
DR PRODOM: PD000357; TGF\_beta; 1.  
DR SMART: SM00204; TGF\_beta; 1.  
DR PROSITE: PS00250; TGF\_BETA; 1.  
KW Glycoprotein.  
SQ SEQUENCE 413 AA: 46303 MW: 4666D12AA1B010 CRC64;

Query Match 29.6%; Score 547; DB 13; Length 413;  
Best Local Similarity 32.3%; Pred. No. 2,4e-44;  
Matches 132; Conservative 59; Mismatches 152; Indels 66; Gaps 11;

OY 5 LLLAFLAPPTVATPRRAGG-----CPACGGPTL--LESORELLDLAKRSILDKLHL 57  
DB 10 LLLGLCWTATRASPPRGEGSVTDCPSALGRLEKAPSSQADMEVAVKHLMLHM 69  
OY 58 TORPTLNPRVSRALRTALQHLH-----GVPOGALLEDN-----RECELIISFAE 103  
DB 70 RSRPTTQPVKPAALLNMIKHLVGVGDGYVEIEDVGRRAERSELEQTSITFAE 129  
OY 104 TGLSTINDTLDHFSSDRTAGDRE-VQOASLMFFVQLPSNTWTTLKVRVLYGPH----- 155  
DB 130 AG-----GSKKVLHFEISKEGSDLSVEQAEFWLFLKLSNRSRTKLITRLVQOQORGO 184  
OY 156 -----GPHNTLTLATQYLLEVDASGMHOLPLGRPAQAACSGHLLTLELVLEG 209  
DB 185 DEERGOEROKKEVLAETKLDLTRSGMHTFNIAKSIQHLDDGKSLDIRIACDOCEGTG 244  
OY 210 ----VILG-----GAA-----HPP--VAARVVGKQHOIHRGIDGCG 243  
DB 245 ATPTLLGKKKKKEEVVKAANGSAGDEERESHRRFLMIMRQSEEHRRRRKRLLEDGK 304  
OY 244 SRMCCROEFVDFREIGHMWTIOPREGVAMNFCIGCCPLHAGMPGTAASFHTAVLNLK 303  
DB 305 VSJCCCKQFVSEFDIGMSWVIAIPGTATNYCEGDCPMYITGSGSGSPFHAIVINDYR 364  
OY 304 ANTAGTGTGGSCCVPFARPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352  
DB 365 MRGYSPTSVKSCCVPFKLRAMSLMYDDGQNIITKKDIONMVEECGCS 413

## RESULT 9

ID 098SP9 PRELIMINARY: PRT: 424 AA.

AC 098SP9; TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE INHIBIN-BETA.  
OS Meleagris gallopavo (Common turkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.  
OX NCBI\_TaxID=9103;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=OVARY;  
RA Ahn J., You S., Kim H., Foster D.N., El Halawani M.E.;  
RT "Molecular cloning of turkey inhibin-alpha and beta subunits."  
RL Submitted (JAN-2001) to the EMBL/Genbank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: AF336338; AAK21265.1; -.  
DR HSSP: P18075; 1BMP.  
DR InterPro: IPR002405; Inhibin\_alpha.  
DR InterPro: IPR000491; Inhibin\_betaa.  
DR InterPro: IPR001318; Inhibin\_betaa.  
DR InterPro: IPR001839; TGF\_beta.  
DR InterPro: IPR001111; TGF\_beta.  
DR Pfam: PR000688; TGF\_beta; 1.  
DR PRINTS: PR00669; INHIBIN.  
DR PRINTS: PR00670; INHIBINB.  
DR PRINTS: PR00672; INHIBINB.  
DR PRODOM: PD000357; TGF\_beta; 1.  
DR SMART: SM00204; TGF\_beta; 1.  
DR PROSITE: PS00250; TGF\_BETA; 1.  
KW Glycoprotein.  
SQ SEQUENCE 424 AA: 47442 MW: B3E7CF3B9DF0C59 CRC64;

Query Match 28.8%; Score 533; DB 13; Length 424;  
Best Local Similarity 30.5%; Pred. No. 5.6e-43;  
Matches 128; Conservative 69; Mismatches 145; Indels 78; Gaps 10;

OY 6 LIAFLAPPTVATPRRAGG-----CPACGGPTL--LESORELLDLAKRSILDKLHL 58  
DB 10 LLIICMIIVSRSPRGSEGHSSVTDCPSALGTLKSDVPSSPEVAVKHLMLHM 69  
OY 59 ORPTLNPRVSRALRTALQHLH-----GVPOGALLEDN-----RECELIISFAE 104  
DB 70 DRPTTQPVKPAALLNMIKHLVGVGDGYVEIEDVGRRAERSELEQTSITFAE 129  
OY 105 GLSTINDTLDHFSSDRTAGDRE-VQOASLMFFVQLPSNTWTTLKVRVLYGPH----- 158  
DB 130 G--TRKKT--LHFEISKEGSELSVEHAEVWLFLKLSNRSRTKLITRLVQOQORGO 184  
OY 159 -----NTNLTALQYLLEVDASGMHOLPLGRPAQAACSGHLLTLELVLEG 203  
DB 185 NSESGEDMEDGKLGERSSETLISEKAVDTKSTNHIIPVSSSVQRLDDGKSLDVRIAC 244  
OY 204 QVAVO-----SSVILG-----GAAHPP--VAARVVGKQHO 232  
DB 245 DLQOETGASLVLLGKKKKKKKDDGEGKEKADAGELTGEERKQSHRRFLMIMRQSEEHRRRRKRLLEDGK 304  
OY 233 IHRGIDCGSGRMCCROEFVDFREIGHMWTIOPREGVAMNFCIGCCPLHAGMPGTAASFHTAVLNLK 303  
DB 305 RRRKGLGDCCKVNICCKKQFVSEFDIGMSWVIAIPGTATNYCEGDCPMYITGSGSGSPFHAIVINDYR 364  
OY 293 SFHTAVNLKANKANAAGTGGSCCVPFARPLSLLYYDRDSNIVKTDIPDMVVEACGCS 352  
DB 365 SFHTAVNLKANKANAAGTGGSCCVPFARPLSLLYYDRDSNIVKTDIPDMVVEACGCS 424

## RESULT 10

09PM65 ID 09PM65 PRELIMINARY: PRT: 404 AA.

AC 09PM65; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ACTININ BETA A PRECURSOR.

OS Carassius auratus (Goldfish).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Carassius.

OX NCBI\_Taxid:7957;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=BRAIN, PITUITARY;

RA Yam K.M., Yu K.L., Ge W.;

RT "Cloning and characterization of actinin beta A subunit.";

RL Mol. Cell. Endocrinol. 0:0-(1999).

CC -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF169032; AAD50448.1; -

DR HSSP: P12643; 3AMP.

DR InterPro: IPR002405; Inhibin\_alpha.

DR InterPro: IPR000491; Inhibin\_beta.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGF-beta.

DR Pfam: PF00019; TGF-beta; 1.

DR PRINTS: PR00688; TGF-beta; 1.

DR PRINTS: PR00669; INHIBINA.

DR PRODOM: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

DR GlycoProtein: Signal.

FT CHAIN 1 23 POTENTIAL.

FT SIGNAL 1 23 ACTIVIN BETA A.

FT CHAIN 289 404

SEQUENCE 404 AA; 44799 MW; 3AFB41BE62A8C0DC CRC64;

Query Match

Best local similarity 28.0%; Score 518; DB 13; Length 404;

Matches 121; Conservative 68; Mismatches 127; Indels 76; Gaps 11;

0Y 14 PTVATPFRAGCGACGAGGTTLESGREL-LDLAKSITDKLHRTPTLNRPVSRAL 72

DB 36 PDDPVP-CPSCALAGROKDESDTDMVEAVKRIHLLNHLNTRPNTHTHPRAAL 90

0Y 73 RTALQHLH-----GVPGALLDNREDECEIISAEGLSTIINOTRIDFH 117

DB 91 LNAIRLHVGRCVGEDGTVEWEDGGGLGEHRESEDEPFLITFAEPG-DAPDKKEDIS 149

0Y 118 FSSDRFAGREVOQASLAFVQLPSNTWTLLKRVVL-----GPHNTNLTAT 166

DB 150 MEGNTLS---VVEQAVWMLLKVAKSGKGVSVOLLGKADPGSADGPOE---AVVS 203

0Y 167 OYLEVDAAGHQLPLGPAQAACSGHLLLEVLGQVAAQSSVIL-----GGA---- 215

DB 204 EKVDTRRSGMHTLPVS-----RTVQTLDDGDSMLSLRVSCPACAEAVPIL 252

0Y 216 -----AHRPFVAARVVGKQHQR--RGIDCGGSRMCCQREFFVDREIG 260

DB 253 VPTESNKKEREQSHRPFMLVYLKPAEHPHRSKRGLECDGKIRVCKRQFVYNEKDIG 312

0Y 261 WHDNIOEGYAMNFCIOCPHLATMGPCIAASFITAVLNLKANTAACTGGSCCVP 320

DB 313 WSDNITLASCYHANYCGEDCSHVASITGSAISFSTVINHRMCGISPFNNKSCCVP 372

0Y 321 ARRLSLLYDRSNIVTIDIPDVVEACGS 352

DB 373 RLRAVSMLYNEEQIKKIDQNMIVEEGCS 404

RESULT 11

09DCG9

PRELIMINARY:

PRT: 115 AA.

AC 09DCG9; 01-MAR-2001 (TREMBlrel. 16, Created)

DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE INHIBIN/ACTIVIN (FRAGMENT).

OS Cyprinus carpio (Common carp).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;

OC Cypriniformes; Cyprinidae; Cyprinus.

OX NCBI\_Taxid:7962;

RN [1]

RP SEQUENCE FROM N.A.

RA Tada T., Hiroo I., Aoki T., Takashima F.;

RT "Cloning and sequencing of carp and medaka activin subunit genes.";

RL Fisheries Sci. 64:680-685(2000).

CC -i- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AB009406; BAB17599.1; -

DR HSSP: P12643; 3AMP.

DR InterPro: IPR002405; Inhibin\_alpha.

DR InterPro: IPR001839; TGF-beta.

DR Pfam: PF00019; TGF-beta; 1.

DR PRINTS: PR00669; INHIBINA.

DR PRODOM: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

DR GlycoProtein: 1

FT NON\_TER 1 1

FT NON\_TER 115 115

SEQUENCE 115 AA; 12666 MW; CD38FA0DD7BD52A6 CRC64;

Query Match

Best local similarity 19.1%; Score 354; DB 13; Length 115;

Matches 61; Conservative 23; Mismatches 28; Indels 6; Gaps 3;

0Y 237 GIDCG-GSRMCCQREFFVDREIGHDWIIQPGYAMNFCIGCPLHIAAGPGIAASFH 295

DB 1 GLECDGTNGCLCCRQGYTIFRLIGNWMIAPAGYGNCGSCPAYLAGVPSASSFH 60

0Y 296 TAVNLNLKATTAAGTTGG--GSCCVPARRPLSLLYDRDSNIVKTDIPDVVEACGC 351

DB 61 TAVNVOYRMR--GMSPGSVNSCIPKILSTMWLYEDDEINIVKRDVPMNIVECGC 115

RESULT 12

09SKP1 ID 09SKP1 PRELIMINARY: PRT: 119 AA.

AC 09SKP1; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)

DE ACTIVIN SUBUNIT A (FRAGMENT).

OS Allurus fulgens (Lesser panda).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.

OX NCBI\_Taxid:9649;

RN [1]

RP SEQUENCE FROM N.A.

RA Wang X., Wang Y.;

RT "Molecular cloning of the activin gene A subunit mature peptide from panda related animals.";

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY029555; AAK40342.1; -

FT NON\_TER 1 1

FT NON\_TER 119 119

SEQUENCE 119 AA; 13328 MW; OA319B2F25D83CB6 CRC64;

Query Match

Best local similarity 19.1%; Score 354; DB 6; Length 119;

Matches 58; Conservative 21; Mismatches 36; Indels 0; Gaps 0;

0Y 237 GIDCGSRMCCQREFFVDREIGHDWIIQPGYAMNFCIGCPLHIAAGPGIAASFH 296

DB 3 GLECDGKVNICKCKQEFVSKDIGMNDWIAPSGYHANYCEGDEPISHIAGTSGSSLSFHS 62

OY 297 AVLNLLKANTAGTTGGCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGC 351  
 DB 63 TVNHVNRGRSGSPFANLKSCCVPTKLRRPSMLYDGGCQNTIKKIDNMIVECCG 117

## RESULT 13

042125 PRELIMINARY: PRT: 119 AA.

AC 042125: PRELIMINARY: PRT: 119 AA.  
 DT 01-JAN-1998 (TREMBlrel. 05, Created)  
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE ACTIVIN BETA B (FRAGMENT).  
 OS Pagrus major (Red sea bream) (Chrysophrys major).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Percoidae;  
 OC Sparidae; Pagrus.  
 OX NCBI\_TaxID=143350;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-OVERT;  
 RA Sakakida Y., Kasahara M., Inaba K.;  
 RT "Analysis of the actinin beta B subunit of Pagrus major."  
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AB006786; BAA22570.1; -.  
 DR HSSP: P12643; 3BMP.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 KW Glycoprotein.  
 FT NON\_TER 1 119  
 FT NON\_TER 119 119  
 SO SEQUENCE 119 AA; 13455 MW; EFB0E9E9AD1FA88 CRC64;

Query Match 19.1%; Score 353.5; DB 13; Length 119;  
 Best Local Similarity 52.2%; Pred. No. 2.2e-26;  
 Matches 60; Conservative 23; Mismatches 27; Indels 5; Gaps 2;

OY 230 KHQHRGIDCGSRMCCROEFFVDREIIGHMDWITIOEGYAMNFCIGCPHIAIGMPG 289  
 DB 8 KHRIRKRLCEDGSSSLCCROQFYIDFLIGNMDWIIAPSGYGNCEGCPAYMAGVPG 67  
 OY 290 IASFTAVLNLLKANTAGTTGG--GSCCVPTARRPLSLLYDRDSNIVKTDIP 342  
 DB 68 SASFTAVVNVQYRMR---GMSPGSVNMSCIPTKLTSMMLYFDDEYIVKRDVP 119

## RESULT 14

09DGF1 PRELIMINARY: PRT: 115 AA.

AC 09DGF1: PRELIMINARY: PRT: 115 AA.  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE INHIBIN/ACTIVIN (FRAGMENT).  
 OS Cyprinus carpio (Common carp).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Cyprinus.  
 OX NCBI\_TaxID=7962;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tada T., Hirose I., Aoki T., Takashima F.;  
 RT "Cloning and sequencing of carp and medaka activin subunit genes."  
 RL Fisheries Sci. 64:680-685(2000).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AB009404; BAB17597.1; -.  
 DR HSSP: P12643; 3BMP.

DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIBIN.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 KW Glycoprotein.  
 FT NON\_TER 1 115  
 FT NON\_TER 115 115  
 SO SEQUENCE 115 AA; 12684 MW; CD38FBBC67BCE316 CRC64;

Query Match 19.1%; Score 353; DB 13; Length 115;  
 Best Local Similarity 51.7%; Pred. No. 2.4e-26;  
 Matches 61; Conservative 23; Mismatches 28; Indels 6; Gaps 3;

OY 237 GIDCGG-GSRMCCROEFFVDREIIGHMDWITIOEGYAMNFCIGCPHIAIGMPG 295  
 DB 1 GLECDGTNGLCRCROQFYIDFLIGNMDWIIAPAGYGNCEGSCPAYMAGVPSASSFH 60  
 OY 296 TAVLNLLKANTAGTTGG--GSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGC 351  
 DB 61 TAVVNOYRMR---GMSPGSVNMSCIPTKLTSMMLYFDDEYIVKRDVPNMIIVECCG 115

## RESULT 15

09DGE6 PRELIMINARY: PRT: 115 AA.

AC 09DGE6: PRELIMINARY: PRT: 115 AA.  
 DT 01-MAR-2001 (TREMBlrel. 16, Created)  
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE INHIBIN/ACTIVIN (FRAGMENT).  
 OS Oryzias latipes (Medaka fish).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Perciformes; Atherinomorpha;  
 OC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.  
 OX NCBI\_TaxID=8090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Tada T., Hirose I., Aoki T., Takashima F.;  
 RT "Cloning and sequencing of carp and medaka activin subunit genes."  
 RL Fisheries Sci. 64:680-685(2000).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AB009409; BAB17602.1; -.  
 DR HSSP: P12643; 3BMP.  
 DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIBIN.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 KW Glycoprotein.  
 FT NON\_TER 1 115  
 FT NON\_TER 115 115  
 SO SEQUENCE 115 AA; 12684 MW; CD38FBBC67BCE316 CRC64;

Query Match 19.1%; Score 353; DB 13; Length 115;  
 Best Local Similarity 51.7%; Pred. No. 2.4e-26;  
 Matches 61; Conservative 23; Mismatches 28; Indels 6; Gaps 3;

OY 237 GIDCGG-GSRMCCROEFFVDREIIGHMDWITIOEGYAMNFCIGCPHIAIGMPG 295  
 DB 1 GLECDGTNGLCRCROQFYIDFLIGNMDWIIAPAGYGNCEGSCPAYMAGVPSASSFH 60  
 OY 296 TAVLNLLKANTAGTTGG--GSCCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGC 351  
 DB 61 TAVVNOYRMR---GMSPGSVNMSCIPTKLTSMMLYFDDEYIVKRDVPNMIIVECCG 115

Search completed: October 12, 2002, 02:08:40

Tue Oct 15 13:49:41 2002

Job time : 45 secs

us-09-684-383-2.rspt

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 22:05:48 : Search time 1932.25 Seconds  
(without alignments)  
16873.397 Million cell updates/sec

Title: US-09-684-383-3  
Perfect score: 1558  
Sequence: 1 AAGGAGTCATCCAGTCGCA.....ATGCCTTAGTCCTCCCTT 1558

Scoring table: IDENTITY-NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08  
Maximum Match 1008  
Listing first 45 summaries

Database : GenBank1:  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_hlg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result Query Match length DB ID Description

1	1558	100.0	1558	6	A48432	A48432 Sequence 3
2	1558	100.0	1558	6	AR038926	AR038926 Sequence
3	1558	100.0	1558	6	AR123395	AR123395 Sequence
4	1547	99.3	1565	10	MMINHACTS	X30819 M. musculus
5	1471.2	94.4	1624	10	MMU95962	U95962 M. musculus
6	1105	70.9	2049	10	MMINBXC2	X30842 M. musculus
7	1037.4	66.6	2433	10	MMACTBC02	U40773 M. musculus
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10	781	50.1	2272	6	AR038925	AR038925 Sequence
11	781	50.1	2272	6	AR123394	AR123394 Sequence
12	781	50.1	2272	6	AR137665	AR137665 Sequence
13	781	50.1	2272	6	HSACTNBC	X82540 H. sapiens m
14	778	49.9	2272	6	AX083554	AX083554 Sequence
15	778	49.9	2272	6	AX137805	AX137805 Sequence
16	555.6	35.7	168473	2	AC063917	AC063917 Homo sapi
17	550.8	35.4	181272	2	AC022506	AC022506 Homo sapi
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19	436.2	28.0	920	10	MMACTBC01	U40772 M. musculus
20	436.2	28.0	1212	10	MMINBXC1	X30841 M. musculus
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22	212.2	13.6	265	5	AR137666	AR137666 Sequence
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24	145	9.3	1749	10	BC010404	BC010404 Mus muscu
25	145	9.3	2125	10	MMU96386	U96386 M. musculus
26	143.4	9.2	687	6	E03666	E03666 DNA sequenc
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28	141.8	9.1	2600	10	AF089825	AF089825 Rattus no
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30	137	8.8	2454	9	BC005161	BC005161 Homo sapi
31	137	8.8	191097	2	AC072033	AC072033 Homo sapi
32	136	8.7	360	6	AR052495	AR052495 Sequence
33	136	8.7	360	6	AR112341	AR112341 Sequence
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35	129.4	8.3	1757	9	HUMINHB2	M31659 Human inhib
36	129.4	8.3	1966	6	101852	101852 Sequence 14
37	129.4	8.3	1966	6	105284	105284 Sequence 25
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39	129.4	8.3	1966	6	164621	164621 Sequence 44
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## ALIGNMENTS

RESULT 1  
LOCUS A48432 1558 bp DNA  
DEFINITION Sequence 3 from Patent WO9601316.  
ACCESSION A48432  
VERSION A48432.1 GI:2302222  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus

REFERENCE  
AUTHORS Hoeltgen, G., Neidhardt, H., Bechtold, R. and Pohl, J.  
TITLE NOVEL GROWTH OR DIFFERENTIATION FACTOR OF THE TGF- beta FAMILY  
JOURNAL Patent: WO 9601316-A 3 18-JAN-1996;  
BIOHARK GRS ZUR BIOTECHNOLOGI (DE)  
COMMENT Other publication AU 2979895 960125  
Other publication DE 19511243 960104.  
FEATURES  
source 1..1558  
/organism="Mus musculus"  
/db\_xref="taxon:10090"

BASE COUNT 340 a 453 c 398 g 367 t





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OY 181 ACTGAACCCAAACCTGAGGCTCCATGCGCAGATGTTGGGGTGCATCTTGAACCTGA 240
DB 181 ACTGAACCCAAACCTGAGGCTCCATGCGCAGATGTTGGGGTGCATCTTGAACCTGA 240
OY 241 GAGCGAGCGGAGCTGCTTCATGATTTGGCCAAAGAAAGTATCCTGAGCAAGCTGACCT 300
DB 241 GAGCGAGCGGAGCTGCTTCATGATTTGGCCAAAGAAAGTATCCTGAGCAAGCTGACCT 300
OY 301 GAGCGAGCGGAGCTGCTTCATGATTTGGCCAAAGAAAGTATCCTGAGCAAGCTGACCT 360
DB 301 GAGCGAGCGGAGCTGCTTCATGATTTGGCCAAAGAAAGTATCCTGAGCAAGCTGACCT 360
OY 361 GCGGCTCCGCGGCTGAGAGGGAACCCCTGTTGAGAGATGACCAAGCAAGAAAGATA 420
DB 361 GCGGCTCCGCGGCTGAGAGGGAACCCCTGTTGAGAGATGACCAAGCAAGAAAGATA 420
OY 421 TGAGATCATGCTTTGCTGACAGACCTCTCCAGCATCAACAGACCCGGCTGAGATT 480
DB 421 TGAGATCATGCTTTGCTGACAGACCTCTCCAGCATCAACAGACCCGGCTGAGATT 480
OY 481 CCACCTCTCTGTAGAAATGAGCAGTGGCATGAGGTCGCGAGACCCGCTTATGTTCTT 540
DB 481 CCACCTCTCTGTAGAAATGAGCAGTGGCATGAGGTCGCGAGACCCGCTTATGTTCTT 540
OY 541 CGTGCAGTTCCCGCACAATGCGCAGACCATGAAATATAGAGTTCTTGTGCTAAGACC 600
DB 541 CGTGCAGTTCCCGCACAATGCGCAGACCATGAAATATAGAGTTCTTGTGCTAAGACC 600
OY 601 ATATGACACCAACCTCAGCTTGAAGTAACTGATACGTGTCAGAGTAAATGCAAGTGGCTG 660
DB 601 ATATGACACCAACCTCAGCTTGAAGTAACTGATACGTGTCAGAGTAAATGCAAGTGGCTG 660
OY 661 GTACAGCTTCTCTGAGGAGCTGAAGCTCAAGCTGCTTGCAGCGAGGAGACCTTACTCT 720
DB 661 GTACAGCTTCTCTGAGGAGCTGAAGCTCAAGCTGCTTGCAGCGAGGAGACCTTACTCT 720
OY 721 GGAGCTGTACCAAGAGCAGTGGCCACAGTCTTCTGATCTGAGGCTGCTTGTCCCA 780
DB 721 GGAGCTGTACCAAGAGCAGTGGCCACAGTCTTCTGATCTGAGGCTGCTTGTCCCA 780
OY 781 CAGGCTTTTGGCAGACCCAGTGAAGGCTTGAAGGAGCAGCATCGGGTCCGCGGAGG 840
DB 781 CAGGCTTTTGGCAGACCCAGTGAAGGCTTGAAGGAGCAGCATCGGGTCCGCGGAGG 840
OY 841 TATGATTCAGAGGGGGGTCAGAGATGCTCTGTCAGCAAGAGTTTGTGAGACTTCCG 900
DB 841 TATGATTCAGAGGGGGGTCAGAGATGCTCTGTCAGCAAGAGTTTGTGAGACTTCCG 900
OY 901 TGAGATTTGGCTGAATGATGATGATCCAGCCCTGAAGGCTATGCAATCTCTGAC 960
DB 901 TGAGATTTGGCTGAATGATGATGATCCAGCCCTGAAGGCTATGCAATCTCTGAC 960
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OY 1081 CTTGCTTACATCTGCGGGGCTCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1140
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DB 1201 TACAGGCTGCTGAGTGAATGAGCTTCTCTGAGAGGAAACTCTGTTCCCACTTCTG 1260

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DB 1321 ACCTTAAGAGAGTCACTAGTACCAAGACCTTTCTCTCTCTGAGACATGTTGACC 1380
OY 1381 CAGTACACCCATCCCTCAGCTTAAATTAGAGGCTAATGAGTCTTACTATATATATGAT 1440
DB 1381 CAGTACACCCATCCCTCAGCTTAAATTAGAGGCTAATGAGTCTTACTATATATATGAT 1440
OY 1441 TTTGTCTTACCAACACCCCTTACTCCCTTACTGACATATGATATCTAGTCTGCTCC 1500
DB 1441 TTTGTCTTACCAACACCCCTTACTCCCTTACTGACATATGATATCTAGTCTGCTCC 1500
OY 1501 CTGACCTGCGCAGGAGGTTCTTATTCAGATGATATGCTTATGTTCTCCCTT 1558
DB 1501 CTGACCTGCGCAGGAGGTTCTTATTCAGATGATATGCTTATGTTCTCCCTT 1558

RESULT 3
AR123395 1558 bp DNA linear PAT 16-MAY-2001
LOCUS AR123395
DEFINITION Sequence 3 from patent US 6171584.
ACCESSION AR123395
VERSION AR123395.1 GI:14108756
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 1558)
AUTHORS Holten, G., Neidhardt, H., Bechtold, R., Pohl, J. and Paulista, M.
TITLE Method of treatment with growth/differentiation factors of the
TGF-beta family
JOURNAL Patent: US 6171584-A 3 09-JAN-2001;
FEATURES
source location/Qualifiers
BASE COUNT 340 a 453 c 398 g 367 t
ORIGIN
Query Match 100.0%; Score 1558; DB 6; Length 1558;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 AAGGATCATGCGCAGTGGAGTCACTGATTCCTCCAGAGGTCCTGTCGCCAGGAC 60
DB 1 AAGGATCATGCGCAGTGGAGTCACTGATTCCTCCAGAGGTCCTGTCGCCAGGAC 60
OY 61 AGAGTTGAAGCAGTCCCGTTGAGACCCCTGAATATAGCTTTGGTCTTTAAGAGGCTA 120
DB 61 AGAGTTGAAGCAGTCCCGTTGAGACCCCTGAATATAGCTTTGGTCTTTAAGAGGCTA 120
OY 121 TCTTCCAGCATGAGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
DB 121 TCTTCCAGCATGAGCTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
OY 181 AGTGAACCCCAAAACTGAGGCTCCATGCCAGATGTTGGGGTGCATCTTGAACCTGA 240
DB 181 AGTGAACCCCAAAACTGAGGCTCCATGCCAGATGTTGGGGTGCATCTTGAACCTGA 240
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DB 241 GAGCGAGCGGAGCTGCTTCATGATTTGGCCAAAGAAAGTATCCTGAGCAAGCTGACCT 300
OY 301 CAGCGAGCGGAGCTTACTGATGAGGCTGAGGCTGAGGAGGCTGAGGAGGCTGAGGAGGCTGGA 360
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DB 361 GCGGCTCCGCGGCTGAGAGGGAACCCCTGTTGAGAGTACCAAGCAAGAAAGATA 420

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DB 601 ATATGACACCAACCTCTGACAGTCAAGTCACTAGCTGAGTGAATGCGAGTGGCTG 660
OY 661 GTACCAAGCTTCTCTGGACCTGAAAGCTCAAGCTGCTTGGACCCAGGACACCTTACTCT 720
DB 661 GTACCAAGCTTCTCTGGACCTGAAAGCTCAAGCTGCTTGGACCCAGGACACCTTACTCT 720
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DB 721 GAGAGCTGTACAGAAAGCCAGAGTGGCCACAGTTCCTGATCCCTGGGCTGTTTCCCA 780
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OY 1501 CTGACCCCTGCCACCGAAGTTCCATTCCAGCATGATATGCTTACTCCCTT 1558
DB 1501 CTGACCCCTGCCACCGAAGTTCCATTCCAGCATGATATGCTTACTCCCTT 1558

RESULT 4
MINHACTS
LOCUS
DEFINITION
ACCESSION
VERSION
X90819.1
KEYWORDS
SOURCE
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Schmitt, J., Holtz, G., Jenkins, N.A., Gilbert, D.J., Copeland, N.G.,
Pohl, J. and Schrewe, H.
Structure, chromosomal localization, and expression analysis of the
mouse inhibin/activin beta C (Inhbc) gene
Genomics 32 (3), 358-366 (1996)
6435913
2 (bases 1 to 1565)
Schrewe, H.
Direct Submission
Submitted (15-AUG-1995) H. Schrewe, Max-Planck-Institut fuer
Immunbiologie, Postfach 1169, D-79011 Freiburg, FRG
Location/Organism
1. 1565
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Best Local Similarity 99.9%; Pired. No. 0;
Matches 1558; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
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 Oy 180 TACTGAACCCCAAACTGAGGGTTCATGACCAGATGTGGGGTGGCCCTCTCTCTCTCT 239  
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 Oy 360 AAGCCCTCCCGGCT 419  
 Db 378 AAGCCCTCCCGGCT 437  
 Oy 420 ATGAGATCATAGCTTGTGTGACACAGAGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 479  
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RESULT 6  
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 LOCUS  
 DEFINITION  
 ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

MMINBXC2  
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 X90842.1 GI:1150507  
 Inhibc gene: Inhibin/activin bc subunit.  
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 Mus musculus.  
 Eukaryote: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:  
 Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus.

REFERENCE  
 1 (bases 1 to 2049)  
 Schrewe, H.  
 Direct Submission  
 Submitted (16-AUG-1995) H. Schrewe, Max-Planck-Institut fuer  
 Immunbiologie, Postfach 1169, D-79011 Freiburg, FRG

TITLE  
 AUTHORS  
 Pohl, J., Hottel, G., Jenkins, N.A., Gilbert, D.J., Copeland, N.G.,  
 Schrewe, H.  
 Structure, chromosomal localization, and expression analysis of the  
 mouse Inhibin/activin beta C (Inhibc) gene

JOURNAL  
 MEDLINE  
 FEATURES  
 96435913

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Best Local Similarity 99.9%; Pred. No. 1.6e-307;  
Matches 1116; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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503 AGTGGCATGAGGTCCGCGAGACCCGCTTCATGTTCTTCGTGACATGCCCCCAATGCC 562  
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683 GAAGCTCAAGCTGCTGCTGACAGTAAATCCCACTGCTGTGTACAGCTTCTCTGGAGCCT 742  
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863 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 922  
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1282 TAGAGTATGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1341  
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VERSION  
KEYWORDS  
SEGMENT  
SOURCE  
ORGANISM

2 of 2  
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 2433)  
Lau, A.L., Nishimori, K. and Matsuzaki, M.  
Structural analysis of the mouse activin beta C gene  
Biochem. Biophys. Acta 1307 (2), 145-148 (1996)  
2 (bases 1 to 2433)  
Lau, A.L.  
Direct Submission  
Submitted (16-NOV-1995) Anthony L. Lau, Pathology, Baylor College  
of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
LOCATION/Qualifiers  
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Matches 1090; Conservative 0; Mismatches 26; Indels 7; Gaps 3;

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DB 95 ACAGACCTCCAGCATCAACAGACCCGCTGAGTCCACTTCTGCTGAGATGGCC 154  
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QY 503 AGTGGCATGAGGTCCGCGAGACCCGCTTCATGTTCTGCTGAGATGCTGCTGCTGCTGCTG 562  
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DB 155 AGTGGCATGAGGTCCGCGAGACCCGCTTCATGTTCTGCTGAGATGCTGCTGCTGCTGCTG 214  
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Db 1221 G 1221

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LOCUS AR038925 2272 bp DNA Linear PAT 29-SEP-1999
DEFINITION Sequence 1 from patent US 5807713.
ACCESSION AR038925
VERSION AR038925.1 GI:5958288
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2272)
AUTHORS Hotten,G., Weidhardt,H., Bechtold,R. and Pohl,J.
TITLE DNA encoding growth/differentiation factor
JOURNAL Patent: US 5807713-A 1 15-SEP-1998;
FEATURES
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ORIGIN

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OY 1224 G 1224
Db 1221 G 1221

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DEFINITION Sequence 1 from patent US 6171584.
ACCESSION AR123394
VERSION AR123394.1 GI:14108755
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2272)
AUTHORS Hotten,G., Weidhardt,H., Bechtold,R., Pohl,J. and Paulista,M.
TITLE Method of treatment with growth/differentiation factors of the
JOURNAL TGF-beta family
PATENT: US 6171584-A 1 09-JAN-2001;
FEATURES
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BASE COUNT 510 a 664 c 512 g 586 t
ORIGIN

Query Match 50.1%; Score 781; DB 6; Length 2272;
Best Local Similarity 79.9%; Pred. No. 5.2e-214;
Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;

OY 28 CACATTCCTCCAGAGGTCCTGTCGTCAGGACAGAGTTGA-AGCACTCCGCTTGAGACC 86
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OY 207 GCCCAGCATTTGGGCTCCATCTTTGACCTGGAGAGCCAGCGGAGCTGCTTCATGANT 266
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DB 324 CTGTGTCCAGAGCTCTTGGAGACTGACAGCCAGCTCCAGGGGGTCCCAAGGGGG 383
OY 387 CCTGTGTGAGCAGTACAGCAGAGACAGAAATATGATATCATCAGCTTGTCTGACAG 446
DB 384 CACTTCTAGAG---GACAAACAGGGAAAGAAATGAAATCATCAGCTTGTCTGAGACAG 440
OY 447 ACCCTCTCAGCATCAACCAAGACCGGCTCGAGTTCACCT---CTCTGTAGAAATGGCCA 503
DB 441 GCCCTCTCAGCATCAACCAAGACTGCTTGTATTTACCTTCTCTGTAGAACTGCTG 500
OY 504 GTGGCATGAGAGGCTCGGAGACCGGCTTCTGCTGCAAGTTCCTCCCAATGGCA 563
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OY 564 CCCAGACCATATATAGAGTCTTGTGCTAAGACCATATAGACACCAACCTCAGCTTGA 623
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VERSION AR137655.1 GI:14479174
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 2272)
AUTHORS
Hotten,G., Neidhardt,H., Bechtold,R. and Pohl,J.
TITLE
DNA sequences encoding growth/differentiation
JOURNAL
Patent: US 6197550-A 2 06-MAR-2001;
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Location/Qualifiers
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source
BASE COUNT 510 a 664 c 512 g 586 t
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Matches 959: Conservative 0: Mismatches 235: Indels 7: Gaps 3:

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 DEFINITION Sequence 3 from Patent WO0111041.  
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 VERSION AX083554.1 GI:13185364  
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 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
 1 (bases 1 to 2272)  
 AUTHORS Hoeften, C., Bechtold, R. and Pohl, J.  
 TITLE Monomeric protein of the tgf- $\beta$ (b) family  
 JOURNAL Patent: WO 011041-A 3 15-FEB-2001;  
 Hygiene AG (CH)

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Query Match 49.9%; Score 778; DB 6; Length 2272;  
 Best Local Similarity 79.6%; Pcore No. 3 8e-213;  
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 QY 87 CTGAATATAGGCTTTGGGCTCTTAAAGAGGCTATCTCCAGAAATGAGCTCTCTTTC 146  
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GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 16:44:11 ; Search time 175.733 Seconds  
(without alignments)  
15221.718 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1469.6	94.3	1837	19	AAV38237 Murine liver activ
2	1025.4	65.8	10708	19	AAV69286 Sequence of mouse
3	779.4	50.0	2272	17	AA71104 Transforming growt
4	778	49.9	2272	22	AA74421 Human TGF-beta M1
5	212.2	13.6	265	14	AAQ4710 TGF-beta-like c1on
6	169.2	10.9	5099	19	AAV38239 Nucleotide sequenc
7	145	9.3	2125	19	AAV38238 Murine liver activ
8	143.4	9.2	687	12	AAQ10891 Encodes Xenopus Bo
9	137	8.8	1616	22	AAK94607 Human full-length

10	137	8.8	2419	17	AA716883 Human growth diff
11	135.4	8.7	1760	19	AAV38240 Human liver activ1
12	129.4	8.3	1966	8	AAV70316 Sequence encoding
13	121	7.8	1530	8	AAV70318 Sequence encoding
14	120.4	7.7	3588	8	AAV70317 Sequence encoding
15	116.4	7.5	1620	22	AAV57530 Human pancreas cel
16	116.4	7.5	1700	22	AAV56008 Angiotensin conver
17	116.2	7.5	1416	22	AAV5491 Sequence encoding
18	116.2	7.5	425	7	AAV60429 Sequence encoding
19	116.2	7.5	958	7	AAV60427 Sequence encoding
20	115.8	7.4	1630	8	AAV70315 Human growth diff
21	115.8	7.4	1873	11	AAQ01648 Encodes Xenopus Bo
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23	93.4	6.0	1667	12	AAQ10890 Tumour suppressor
24	74.6	4.8	8513	22	AAV45354 Human bone morphog
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## ALIGNMENTS

AAV38237	AAV38237 standard; cDNA; 1837 BP.
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01-FEB-1999	(first entry)
Murine liver activin beta c polypeptide encoding cDNA.	
Liver activin: beta c; beta e; cell differentiation; haematopoiesis;	
erythroid; ovarian follicular maturation; hormone; neuronal survival;	
spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;	
osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassy;	
menstrual disorder; transgenic; modulator; ss.	
Mus sp.	
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28-MAY-1998.	
20-NOV-1997;	97WO-US20882.







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RESULT 3  
AA111104

ID AA111104 standard; cDNA: 2272 BP.

AC AA111104;

XX 09-AUG-1996 (first entry)

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DE Transforming growth factor beta MP-121 cDNA.
XX
XX TGF-beta; MP-121; mitogen; differentiation; induction; promotion;
KW maintenance; morphogen; tissue regeneration; dental implantation;
KW wound healing; ss.
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XX Homo sapiens.
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XX FT /product= TGF-beta_MP-121
XX FT 836..1183
XX FT /*lag- b
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XX 04-JAN-1996.
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XX 27-MAR-1995; 95DE-1011243.
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XX 01-JUL-1994; 94DE-1423190.
XX
XX (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX Bechtold R, Neidhardt H, Pohl J, Hoelten G;
XX WPI: 1996-050788/06.
XX P-ESDB: AAR89729.
XX
XX DNA encoding transforming growth factor beta MP-121 - has mitogenic
XX and differentiation-inducing activity, e.g. for use in wound healing
XX
XX Claim 1; Page 10; 15pp; German.
XX
XX A cDNA library prepared using total RNA from human liver was
XX subjected to PCR amplification using primers corresp. to conserved
XX regions within the TGF-beta family. Amplification products were
XX subcloned and sequenced. One clone (designated pSK-MP121) was found
XX to contain a new sequence. Part of the insert from this clone was
XX used to re-screen the human liver cDNA library and a 2272 bp fragment
XX (i.e. the present sequence) coding for a TGF-beta-like protein was
XX isolated. The protein encoded by the cDNA insert has mitogenic and
XX differentiation-inducing properties making it (or fusion proteins
XX comprising it or heterodimers of the protein with a cysteine knot
XX motif protein) useful for inducing tissue regeneration.
XX
XX Sequence 2272 BP; 510 A; 663 C; 513 G; 586 T; 0 other:
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XX Best Local Similarity 79.8%; Pred. No. 3.2e-218;
XX Matches 958; Conservative 0; Mismatches 236; Indels 7; Gaps 3;
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XX DB 24 CACATTCCTCCAGGTCCTGTCGTCAGGACAGAGTGAAGCAGCTTTAGACC 83
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OY 147 TCTGGCTCTCTGTTGCTGACCTCAACACAGTAGTGAACCCCAAACTGAGGCTCAT 206
Db 144 TTCTGGCTTCTCTCTCTGCTGCTCCACACAGTGGCCACTCTCCAGAGCTGCGTCACT 203
OY 207 GCCCAGCATGTTGGGGTGCATCTTTGACCTGAGAGCCAGCGGAGCTTCTCGATT 266
Db 204 GTCCAGCATGTTGGGGGCCCCACCTTGGAACTGGAGAGCCAGCGGAGCTCTTCTGATC 263
OY 267 TGGCCAGAAAGATGCTGACAAAGCTGCACTTACGACGCGGCCCATCTACTGCTGCGC 326
Db 264 TGGCCAGAAAGATGCTTGGAGAGCTGCACTTACGACGCGGCCCATCTACTGCTGCGC 323
OY 327 CAGTGTCCAGAGGGCTCTCAGACGCGGCTGCGAGCGGCTCCGGGCTCGACGGGAAA 386
Db 324 CTGTGTCCAGAGGCTCTTGAAGAGCTGCACTTACGACGCGGCCCATCTACTGCTGCGC 383
OY 387 CCTGTGTGAGCATGACAGACAGACAGAAATATGATCATGCTTGTGCTGACAGAG 446
Db 384 CACTTCTAGAG---GACAAACAGGGAACAGGATGTGAATCATCTGCTGAGACAG 440
OY 447 ACCTCTCCAGCATCAACGACAGCCGCTGCTGATCTCACTT---CTCTGTGAATAGGCA 503
Db 441 GCTCTCCACCATCAACGACAGCTGCTGATTTTCACTTCTCTGATGAGAACTGTGTG 500
OY 504 GTGGCATGAGAGTCCGCGAGACCGGCTTCACTGCTGCGAGCTTCCCAAGATGCA 563
Db 501 GTGACAGGAGAGTCCAGACAGGCGCACTCTCATGTTCTTGTGACAGCTCCCTTCAATACA 560
OY 564 CCCAGACCATGAATATAGAGTCTTGTGCTAAGACCATATGACACCAACCTGCACTGA 623
Db 561 CTTGAGACCTTGAAGATGAGAGTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 620
OY 624 CAGTGTGAGAGTGGTGGAGTGAATGCCAGTGGCTGATGACAGCTTCTGCGAGCTG 683
Db 621 CTACTGATGATCTGCTGGAGTGGATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 680
OY 684 AAGCTCAAGCTTGTGACAGCAGGACGACCTTACTGCTGCTGCTGCTGCTGCTGCTG 743
Db 681 AAGCTCAAGCTGCTGACAGCAGGAGGACCTGACCTGAGCTGCTGCTGCTGCTGCTG 740
OY 744 TGGCCCAAGTCTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803
Db 741 TAGCCCAAGCTCTGATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800
OY 804 TAAGGTTGAGGGAAGATGAGGCTTGGCGGCGAGGATGATGATGCTGCAAGGAGTCCA 863
Db 801 TGAAGTTGAGGGAAGATGAGGCTTGGCGGCGAGGATGATGATGCTGCAAGGAGTCCA 860
OY 864 CGATGCTGCTGACAGAGATTTTGTAGACTTCCGAGATTTGGCTGGAATGACTGCA 923
Db 861 GGATGCTGCTGACAGAGATTTTGTAGACTTCCGAGATTTGGCTGGAATGACTGCA 920
OY 924 TCAATCCAGCTGAGAGCTATGCACTTCTGCACTGCGAGGCGGCACTACATGCTG 983
Db 921 TCAATCCAGCTGAGAGCTATGCACTTCTGCACTGCGAGGCGGCACTACATGCTG 980
OY 984 CAGGATGCGCTGAGATCTGCTGCTCTTTCACATGCACTGCTGATGCTGCAAGGCA 1043
Db 981 CAGGATGCGCTGAGATCTGCTGCTCTTTCACATGCACTGCTGATGCTGCAAGGCA 1040
OY 1044 ACCGATGCTGCTGAGCAGCTGCGAGGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1103
Db 1041 ACAGACTGCTGAGCAGCAGCTGAGGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1100
OY 1104 TGTCTTGTCTCTATGATGAGAGGAGACAGCAATGCTCAAGAGAGGATATGATGACATG 1163
Db 1101 TGTCTTGTCTCTATGATGAGAGGAGACAGCAATGCTCAAGAGAGGATATGATGACATG 1160

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OY 1164 TGTGTCAGAGGCTGCGGGCTGTTAGTACTTATGAGTGAATACAGGCTGCTGAGTGAATG 1223
Db 1161 TAGTAGAGGCTGTGGGTGTCAGTAGTATGATGATGATGATGATGATGATGATGATG 1220
OY 1224 G 1224
Db 1221 G 1221

RESULT 5
AA047710
ID AA047710 standard; cDNA to mRNA; 265 BP.
XX
AC AA047710;
XX
DE 11-FEB-1994 (first entry)
XX
DE TGF-beta-like clone MP-121.
XX
KW Human; transforming growth factor; beta; TGF-beta; pharmaceutical;
KW bone; cartilage; tooth; wound repair; immunosuppressor;
KW organ transplant; cosmetic surgery; antibody; diagnosis; ss.
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 2..265
FT /tag= a
XX
XX W09316099-A.
XX
XX 12-FEB-1993; 93WO-EP00350.
XX
XX 12-FEB-1992; 92EP-0102324.
XX
PA (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.
XX
XX Hoelten G, Neidhardt H;
XX
XX WPI: 1993-272824/34.
XX
XX P-PSDB: AAR45447.
XX
PT New transforming growth factor-beta family proteins and DNA -
PT used in fissure and wound repair, in treatment of bone, cartilage
PT and tooth defects, and antibodies for diagnosis
XX
PS Claim 4: Page 18: 29pp; English.
XX
CC The sequences given in AA047709-10 represent embryo and liver derived
CC human transforming growth factor-beta (TGF-beta) genes respectively.
CC The proteins encoded by these sequences may be used in a pharmaceutical
CC composition for the treatment of various bone, cartilage or tooth
CC defects and in tissue and wound repair processes. These proteins
CC may also be used as immunosuppressors in organ transplants and in
CC cosmetic surgery. Antibodies raised against these proteins may be
CC used for diagnostic purposes.
SQ
Sequence 265 BP; 58 A; 80 C; 69 G; 58 T; 0 other;

Query Match 13.6%; Score 212.2; DB 14; Length 265;
Best Local Similarity 87.5%; Pred. No. 4e-52;
Matches 232; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

OY 925 CATCCAGCCTGAGGCTATGAGCCATGAACTTGCACACTGCGGCACTGCTGCTGCTGCTG 984
Db 1 CATCCAGCCTGAGGCTATGAGCCATGAACTTGCACACTGCGGCACTGCTGCTGCTGCTG 60
OY 985 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1044
Db 61 AGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 120

```













KW	Fertility control; contraception; hormone; spermatogenesis; ss.
XX	Homo sapiens.
OS	
XX	
PH	Key
FT	CDS
FT	Location/Qualifiers
FT	/tag= b
FT	/product-hydrophobic signal sequence a pro-region
FT	717..1061
FT	/tag= b
XX	
PN	EP222491-A.
XX	
PD	20-MAY-1987.
XX	
PF	02-OCT-1986; 86EP-0307586.
XX	
PR	12-SEP-1986; 86US-0906729.
PR	03-OCT-1985; 85US-0783910.
PR	10-FEB-1986; 86US-0827710.
XX	
PA	(GETH ) GENENTECH INC.
PI	Mason AJ, Secburg PH;
DR	WPI: 1987-137512/20. P-PSTDB: AAP70204.
XX	
PT	Recombinant human or porcine inhibin or activin - used for modulating clinical condition or reproductive physiology of animals.
PS	Disclosure; Fig 9A; 48pp; English.
XX	
CC	A compsn. comprising human or porcine inhibin which is completely free of unidentified or porcine proteins is claimed. Also claimed are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta chain. Sequencing of inhibin-encoding cDNA has led to the identification of prodomain regions located N-terminal to the c mature inhibin chains that represent coordinately expressed biologically active polypeptides. The prodomain regions or prodomain immunogens are useful in monitoring preproinhibin processing in transformant cell culture or in experiments directed at modulating the clinical condn. or reproductive physiology of animals.
CC	
CC	
XX	
SO	Sequence 1966 BP: 424 A: 557 C: 621 G: 364 T: 0 other:
	Query Match 8.3%; Score 129.4; DB 8; Length 1966; Best Local Similarity 58.9%; Pred. No. 2..2e-27; Matches 261; Conservative 0; Mismatches 176; Indels 6; Gaps
OY	743 GTGGCCACAGTTCCTTGATCCTGCGCTGTGTTCCACAGGCCCTTTGTGGCACGCCAG 802
Db	618 GTGCCTCCGCTGCTTCTGCACCAGCAAGAGTCGACCGCTTGTGTGTGCAG 677
OY	803 GTAAG---GCTTGAGGGCAAGCATCGGGTTCGCCGGGAGATTATGCACGGGGG 859
Db	678 GCTCGGCTGGCGACAGCAGCAGCCGATTTCGCAAGCGAGGCTGGAGTGGCGCG 737
OY	860 TCACAGATGCTGCTGCAGCAAGATTTTTTGTAGACTTCCGTGAATTTGGCTGAATGAC 919
Db	738 ACCAACTCTGTTGGCAGCAAGATTCTTCATTACTTCGCCCTCATGGGCTGGAACGAC 797
OY	920 TGATCATCAGCGCTGAAGCTATGCAATGAACTTCTGCACCTGGCAGTGGCCACTACAT 979
Db	798 TGGATCATGACACCAACCGGCTACTACGGCAACTACTGAGGCGACGACGCCAGCTAC 857
OY	980 GTGGCAGGCATGCTGCGCATCTTGCTCTTTACACTGCAGTGTGTAATCTGCTCAA 1039
Db	858 CTGGCAGGGGCTCCCGGCTCTGCTCTTCCTTCACACAGGCGTGTGTAACAG---TAG 914
OY	1040 GCCAACGACACTCTCTGGCACACACTGAGGAGGGCTGTCTGTGCTGCTCATCTGCGCG 1099

```

Db      915  CGCATGCGGGGCTCTGAACCCCGGACACGGTGAACCTCCCTGCTGGCATTCGACACCACTGAGC 974
Oy      1100  CCTCTGCTTTGCTCTACTATGACAGGACAGACACATTCTCAACAGCATATACCTGAC 1159
Db      975  AOCATGCTCATCTGACTTGCATGTAGTACACATACGTCTCAAGCGGAGCGTCCCAAC 1034
Oy      1160  ATGTGTGTCGAGCGCTGCGGGTG 1182
Db      1035  ATGATTGTGACGAGTGC GGCTG 1057

RESULT 13
ID      AAN70318  AAN70318  standard; cDNA; 1530 BP.
XX
XX      AAN70318;
AC
XX      09-APR-1991  (first entry)
DE
XX      Sequence encoding porcine inhibin beta-chain precursor beta-B.
XX      Fertility control; contraception; hormone; spermatogenesis; ss.
OS      Sus scrofa domestica.
XX
XX      Key      Location/Qualifiers
FH      CDS      1..810
FT      /tag- a
FT      /product=hydrophobic signal sequence a pro-region
FT      mat_peptide 811..1160
FT      /*tag- b
XX
XX      EP222491-A.
XX
XX      20-MAY-1987.
XX
XX      02-OCT-1986; 86EP-0307586.
XX
XX      12-SEP-1986; 86US-0906729.
XX      03-OCT-1985; 85US-0783910.
XX      10-FEB-1986; 86US-0827710.
XX
XX      (GETH ) GENENTECH INC.
XX
XX      Mason AJ, Seeburg PH;
XX
XX      WPI: 1987-137512/20.
XX      P-PSDB; AAP70201.
XX
XX      Recombinant human or porcine inhibin or activin - used for
XX      modulating clinical condition or reproductive physiology of
XX      animals.
XX
XX      Disclosure; Fig 1B; 48pp; English.
XX
XX      A compsn. comprising human or porcine inhibin which is completely
XX      free of unidentified or porcine proteins is claimed. Also claimed
XX      are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
XX      chain. Sequencing of inhibin-encoding cDNA has led to the
XX      identification of prodomain regions located N-terminal to the
XX      mature inhibin chains that represent coordinately expressed
XX      biologically active polypeptides. The prodomain regions or
XX      prodomain immunogens are useful in monitoring preproinhibin
XX      processing in transformant cell culture or in experiments directed
XX      at modulating the clinical cond. or reproductive physiology of
XX      animals.
XX
XX      Sequence 1530 BP; 318 A; 469 C; 511 G; 232 T; 0 other;
XX
Query Match      7 8%; Score 121; DB 8; Length 1530;
Best Local Similarity 56.2%; Pred. No. 5.7e-25;
Matches 251; Conservative 0; Mismatches 190; Indels 6; Gaps 1;

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OY 743 GTGSCCAGACATCTGCTGATCTGGGCTGTTTCCACAGACCTTTTGGCAGCCAG 802
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 604 GTGCTGCCCCGTTTGTGGACCCGCGGCGAGAGATCACCACCCCTTCTGTGTGACAG 663
OY 803 GTAAAGGTTGAGGCCA-----ACCATGCGGTTCCCGCGAGATGATGATGGCCAGGG 856
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 664 GCGGACATGGGTGACAGACAGCCACCGCATCCGCAAGCGGGGCTGAGTGTGACGGC 723
OY 857 GGGTCCAGGATGTCTCTCCAGACAGATTTTGTAGACTTCCGAGATTGGCTGGAAT 916
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 724 CGGACCAACCTGTGTTCAGAGCAACAGTTTCAATCCAGCTTCCGCTCATTTGGCGTAGT 783
OY 917 GACATGATCCAGCCTGAAAGGCTATGCCATGAACTTCTGACATGGGACAGTCCCACTA 976
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 784 GACTGCTATCCGCGCCACCGGCTATGGAATGGAATCTGAGGCGCTGTCGCCGC 843
OY 977 CATGTGGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1036
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 844 TACCTGGCAGGAGGCTGCGAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 903
OY 1037 AAGCCACAGCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1096
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 904 CGCATGCGGCGCTGAAACCGCTGCGGACAGTGAATCTGCTGCTGCTGCTGCTGCTGCTG 963
OY 1097 CGCCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1156
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 964 AGCAGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1023
OY 1157 GACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1183
    ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1024 AACATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1050

```

## RESULT 14

AAH70317 standard; cDNA: 3588 BP.

```

XX AC AAH70317;
XX DT 09-APR-1991 (first entry)
XX DE Sequence encoding porcine inhibin beta-chain precursor beta-A.
XX KW Fertility control; contraception; hormone; spermatogenesis; ss.
XX OS Sus scrofa domestica.
XX FH Key Location/Qualifiers
XX FT CDS 34..957
XX FT mat_peptide /product=hydrophobic signal sequence a pro-region
XX FT polyA_signal /tag= b
XX FT /tag= 3551..3556
XX FT /tag= c
XX PN EP222491-A.
XX PD 20-MAY-1987.
XX PF 02-OCT-1986; 86BP-0307586.
XX PR 12-SEP-1986; 86US-0906729.
XX PR 03-OCT-1985; 85US-0783910.
XX PR 10-FEB-1986; 86US-0827710.
XX PA (GETH ) GENENTECH INC.
XX PT Mason AJ, Seeburg PH;
XX DR WPI: 1987-137512/20.
XX FR P-PDB: AAP70200.

```

```

XX XX
XX PT Recombinant human or porcine inhibin or activin - used for
XX PT modulating clinical condition or reproductive physiology of
XX PT animals.
XX PS Disclosure: Fig 1B; 48bp; English.
XX PS
XX CC A compsn. comprising human or porcine inhibin which is completely
XX CC free of unidentified or porcine proteins is claimed. Also claimed
XX CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta
XX CC chain. Sequencing of inhibin-encoding cDNA has led to the
XX CC identification of prodomain regions located N-terminal to the
XX CC mature inhibin chains that represent coordinately expressed
XX CC biologically active polypeptides. The prodomain regions or
XX CC prodomain immunogens are useful in monitoring preproinhibin
XX CC processing in transformant cell culture or in experiments directed
XX CC at modulating the clinical cond. or reproductive physiology of
XX CC animals.
XX SQ

```

Sequence 3588 BP; 881 A; 986 C; 998 G; 723 T; 0 other;

Query Match 7.7%; Score 120.4; DB 8; Length 3588;

Best Local Similarity 57.4%; Pred. No. 1.3e-24;

Matches 217; Conservative 0; Mismatches 161; Indels 0; Gaps 0;

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OY 812 GAGGCAACATCGGGGTTGGCGGAGGATGATTTGCCAGGGGGGCTCAGATGTC 871
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 931 GAGCACCCCAACCGCCGCGGCGGCTGAGTGCAGCGCAAGTCAATCTGC 990
OY 872 TCTGCAGAGAGTTTGTAGACTTCCGTGAGATTGGCTGATGATGATCAG 931
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 991 TGTAGAAAGCACTTCTTGTCAAGTTTCAAGGACATGCGGTGGAACGATGATTCGT 1050
OY 932 CCTGAAGCTATGCCATGAACTTCTGCACTGGGCACTGCCACTACATGTGGAGCATG 991
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1051 CCGTCCGCTTACCCAGCCCAACTGACGAGCGAGTGGTCCCGCCACATAGCGGGCAGC 1110
OY 992 CCGTGCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1051
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1111 TCGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1170
OY 1052 GCTGGCACCACATGCGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1111
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1171 AGCCCTTTCGCCAACCCTGAAAGTGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1230
OY 1112 CTCTACTATGACAGGACAGCAACATTTGCAAGAGGATATTAAGTGTGTGAG 1171
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1231 CTGTAAGTACAGAGAGGAGGAGCAATCATCAAGAGGACATCCAGAAATGATCGTGAG 1290
OY 1172 GCTGCGGGGTGATTAG 1189
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1291 GAGTGGGGTCTCTAG 1308

```

## RESULT 15

AAH57530 standard; cDNA: 1620 BP.

```

XX AC AAH57530;
XX DT 10-SEP-2001 (first entry)
XX DE Human pancreas cell specific cDNA sequence SEQ ID NO:370.
XX DE
XX KW Human; tissue specific; diagnosis; brain; heart; skeletal muscle;
XX KW lung; liver; uterus; ovary; stomach; intestine; kidney; pancreas; ss.
XX KW metabolic disease; developmental disease; cytostatic; immunomodulatory;
XX KW neuroprotective; gene therapy; cancer; immunopathology; neuropathology.
XX OS Homo sapiens.
XX PN WO200132927-A2.

```



2  
1  
1  
1

200

GenCore version 5.1.3  
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OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 16:51:16 : Search time 36.2042 Seconds  
(without alignments)  
10570.520 Million cell updates/sec

Title: US-09-684-383-3  
Perfect score: 1558  
Sequence: 1 AAGGAGTCATCCAGTCGGA.....ATGCCCTAGTCTCCCTT 1558

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
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2: /cgn2\_6/ptodata/1/lna/5B\_COMB.seq.\*  
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6: /cgn2\_6/ptodata/1/lna/Backfillseq.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed.  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1558	100.0	1558	1	US-08-482-577B-3
2	1558	100.0	1558	1	US-09-218-176-3
3	781	50.1	2272	1	US-08-482-577B-1
4	781	50.1	2272	3	US-08-289-322E-2
5	781	50.1	2272	4	US-09-218-176-1
6	781	50.1	2272	4	US-09-054-526B-2
7	212.2	13.6	265	3	US-08-289-322E-5
8	212.2	13.6	265	4	US-09-054-526B-5
9	143.4	9.2	687	1	US-08-455-550-2
10	137	8.8	2419	2	US-08-765-662-13
11	137	8.8	2419	5	PCT-US95-08745-13
12	136	8.7	360	2	US-08-274-215A-11
13	136	8.7	360	2	US-08-765-662-11
14	136	8.7	360	2	US-09-184-933-11
15	136	8.7	360	5	PCT-US95-08745-11
16	129.4	8.3	1966	1	US-08-197-792-44
17	129.4	8.3	1966	1	US-08-459-850-44
18	129.4	8.3	1966	1	US-08-459-850-44
19	129.4	8.3	1966	1	US-08-459-850-44
20	127	8.2	1524	1	US-08-197-792-34
21	127	8.2	1524	1	US-08-459-850-34
22	120.4	7.7	3588	1	US-08-197-792-32
23	120.4	7.7	3588	1	US-08-459-850-32
24	120.4	7.7	3588	1	US-08-459-850-32
25	116.4	7.5	1633	1	US-08-197-792-42
26	116.4	7.5	1633	1	US-08-459-850-42
27	116.4	7.5	1633	1	US-08-459-850-42

28	93.4	6.0	1667	1	US-08-455-550-1	Sequence 1, Appl1
29	70.4	4.5	926	1	US-08-362-670B-1	Sequence 1, Appl1
30	70.4	4.5	926	3	US-08-333-576C-1	Sequence 1, Appl1
31	70.4	4.5	926	4	US-08-808-324-1	Sequence 1, Appl1
32	70.4	4.5	926	5	PCT-US94-14030A-1	Sequence 1, Appl1
33	70.4	4.5	1345	1	US-08-362-670B-33	Sequence 33, Appl1
34	70.4	4.5	1345	3	US-08-333-576C-33	Sequence 33, Appl1
35	70.4	4.5	1345	4	US-08-808-324-33	Sequence 33, Appl1
36	70.4	4.5	1345	5	PCT-US94-14030A-33	Sequence 33, Appl1
37	68.2	4.4	420	1	US-08-360-914B-11	Sequence 11, Appl1
38	68.2	4.4	420	1	US-08-741-589A-11	Sequence 11, Appl1
39	68.2	4.4	420	5	PCT-US94-13181-11	Sequence 11, Appl1
40	68.2	4.4	1003	1	US-07-800-364B-13	Sequence 13, Appl1
41	68.2	4.4	1003	2	US-07-989-847-11	Sequence 11, Appl1
42	68.2	4.4	1003	4	US-08-469-411-11	Sequence 11, Appl1
43	68.2	4.4	1723	1	US-07-843-646-28	Sequence 28, Appl1
44	68.2	4.4	1723	1	US-07-901-703-10	Sequence 10, Appl1
45	68.2	4.4	1723	1	US-08-147-023-28	Sequence 28, Appl1

## ALIGNMENTS

RESULT 1  
US-08-482-577B-3  
Sequence 3, Application US/08482577B  
Patent No. 5807713  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSER: NIKAIIDO, MARCELSTEIN, MURRAY, AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1558 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
US-08-482-577B-3  
Query Match 100.0%; Score 1558; DB 1; Length 1558;  
Best Local Similarity 100.0%; Pred. No. 0;



Matches 1558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
OY 1 AAGAGTCATGCCAGTGGAGGTGACATTCCTCCAGGAGTCCCTGTGCCAGAC 60
  |||
Db 1 AAGAGTCATGCCAGTGGAGGTGACATTCCTCCAGGAGTCCCTGTGCCAGAC 60
OY 61 AAGAGTCATGCCAGTGGAGGTGACATTCCTCCAGGAGTCCCTGTGCCAGAC 120
  |||
Db 61 AAGAGTCATGCCAGTGGAGGTGACATTCCTCCAGGAGTCCCTGTGCCAGAC 120
OY 121 TCCCTCAGCAATGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
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Db 121 TCCCTCAGCAATGAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
OY 181 AGTGAACCCCAAACTGAGGCTCCATGCCAGCATGTTGGGTCGCATCTTGACCTGA 240
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Db 181 AGTGAACCCCAAACTGAGGCTCCATGCCAGCATGTTGGGTCGCATCTTGACCTGA 240
OY 241 GAGCCAGGGAGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
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Db 241 GAGCCAGGGAGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 300
OY 301 CAGCCAGGGAGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
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Db 301 CAGCCAGGGAGCTGCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 360
OY 361 GCGCCCTCCCGGGCTCTGAGGAGGAAACCTGTTGGAGCATGACAGACAGAGATA 420
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Db 361 GCGCCCTCCCGGGCTCTGAGGAGGAAACCTGTTGGAGCATGACAGACAGAGATA 420
OY 421 TGAGATCATGAGTCTGTCAGACAGACCTCTCAGCATCAACAGACCCGGCTGAGTT 480
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Db 421 TGAGATCATGAGTCTGTCAGACAGACCTCTCAGCATCAACAGACCCGGCTGAGTT 480
OY 481 CCACCTCTCTGAGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
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Db 481 CCACCTCTCTGAGTGAATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
OY 541 CGTGCAGTTCCTCCAGCAATGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
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Db 541 CGTGCAGTTCCTCCAGCAATGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
OY 601 ATATGACACCAACCTGACCTGTCAGACAGTCTGAGTGTGAGGAGTGAATGAGGAG 660
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Db 601 ATATGACACCAACCTGACCTGTCAGACAGTCTGAGTGTGAGGAGTGAATGAGGAG 660
OY 661 GTACAGGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
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Db 661 GTACAGGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
OY 721 GAGGCTGTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
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Db 721 GAGGCTGTACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
OY 781 CAGGCTCTCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
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OY 841 TATGATTCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 900
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OY 901 TGAGATTCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
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Db 901 TGAGATTCGCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 960
OY 961 TGGCAGTGGCCACTACATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
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Db 961 TGGCAGTGGCCACTACATGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1020
OY 1021 AGTGCATGATTCGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
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Db 1021 AGTGCATGATTCGTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1080
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OY 1081 CGTGCTACATCTCGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
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Db 1081 CGTGCTACATCTCGGCGCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
OY 1141 CAAGAGGATATACCTGACATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
  |||
Db 1141 CAAGAGGATATACCTGACATGAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1200
OY 1201 TACAGGCTGCTGAGGATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
  |||
Db 1201 TACAGGCTGCTGAGGATGAGATGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1260
OY 1261 TCCAGATGGAACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
  |||
Db 1261 TCCAGATGGAACACCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1320
OY 1321 ACCTCTAAAGAGAGTCTAGTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
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Db 1321 ACCTCTAAAGAGAGTCTAGTACCAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1380
OY 1381 CAGTACACCCATCTCTAGGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1440
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Db 1381 CAGTACACCCATCTCTAGGCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 1440
OY 1441 TTTGCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
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Db 1441 TTTGCTCTAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1500
OY 1501 CTGAGCCCTGCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1558
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Db 1501 CTGAGCCCTGCAACCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1558
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RESULT 2  
US-09-218-176-3  
Sequence 3, Application US/09218176  
Patent No. 6171584  
GENERAL INFORMATION:  
APPLICANT: H THEN, Gertrud  
APPLICANT: NEIDHARDT, Helge  
APPLICANT: BECHTOLD, Rolf  
APPLICANT: POHL, Jens  
APPLICANT: PAULISTA, Michael  
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIKAIIDO, MARWELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., G Street Lobby,  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/218,176  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,048  
FILING DATE: 12-JUL-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCW/EP96/03065  
FILING DATE: 12-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350

1 FILING DATE: 2-FEB-1993  
 2 PRIOR APPLICATION DATA: 1993  
 3 APPLICATION NUMBER: US 08/482,577  
 4 FILING DATE: 7-JUN-1995  
 5 PRIOR APPLICATION DATA:  
 6 APPLICATION NUMBER: EP 92 102 324.8  
 7 FILING DATE: 12-FEB-1992  
 8 PRIOR APPLICATION DATA:  
 9 APPLICATION NUMBER: DE P 44 23 190.  
 10 FILING DATE: 01-JUL-1994  
 11 PRIOR APPLICATION DATA:  
 12 APPLICATION NUMBER: DE 195 11 243.1  
 13 FILING DATE: 27-MAR-1995  
 14 ATTORNEY/AGENT INFORMATION:  
 15 NAME: KITTS, Monica Chin  
 16 REGISTRATION NUMBER: 36,105  
 17 REFERENCE/DOCKET NUMBER: P564-6010  
 18 TELECOMMUNICATION INFORMATION:  
 19 TELEPHONE: 202/638-5000  
 20 TELEFAX: 202/638-4810  
 21 INFORMATION FOR SEQ. ID NO.: 3:  
 22 SEQUENCE CHARACTERISTICS:  
 23 LENGTH: 1558 base pairs  
 24 TYPE: nucleic acid  
 25 STRANDEDNESS: single  
 26 TOPOLOGY: linear  
 27 MOLECULE TYPE: DNA  
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APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MARCELSTEIN, MURRAY, AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELEPHONE: 202/638-4810  
TELEFAX: 202/638-5000  
INFORMATION FOR SEQ. ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2272 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA  
US-08-482-577B-1

Query Match 50.1%; Score 781; DB 1; Length 2272;  
Best Local Similarity 79.9%; Pred. No. 3,46-229;  
Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;

QY 28 CACATTCCTCCAGAGGCTCCCTGCGCCAGAGAGTTGA-AGCAGCTCCCTTGAGACC 86  
DB 24 CACACTTCCTCCAGAGGCTCCCTGCGCCAGAGAGTTGA-AGCAGCTCCCTTGAGACC 83  
QY 87 CTGAATATATAGGCTTTGGGCTCTTAAAGAGGCTTATCCAGCAATGGGCTCTCTGCG 146  
DB 84 CTGAGGCTCTGAGTCTGTATGCTCAAGAGAGGCTTCCAGCAATGAGCTCTCTATTTGC 143  
QY 147 TCTTGCTCTCTGTTCTGCTGACTCAACACAGTATGAGAACCCCAAACTGAGGTCAT 206  
DB 144 TCTTGCTCTCTGTTCTGCTGACTCAACACAGTATGAGAACCCCAAACTGAGGTCAT 203  
QY 207 GCCCAGCATGTTGGGCTGCTTGAACCTGAGAGAGCCAGGAGGCTGCTTCTGAT 266  
DB 204 GTCCAGCATGTTGGGCTGCTTGAACCTGAGAGAGCCAGGAGGCTGCTTCTGAT 263  
QY 267 TGGCCAGAAAGTATCTTGGAGCAAGCTGACCTCAGCAGCCAGCCCTTACTGATGCGC 326  
DB 264 TGGCCAGAAAGTATCTTGGAGCAAGCTGACCTCAGCAGCCAGCCCTTACTGATGCGC 323  
QY 327 CAGTGTCCAGAGGCTCTCAAGAGCCGCTGAGGCTCCGCGGCTGAGAGGGA 386  
DB 324 CTGTGTCCAGAGGCTCTCAAGAGCCGCTGAGGCTCCGCGGCTGAGAGGGA 383  
QY 367 CCCTGTGAGCATGACAGAGACAGAAAGATATGAGATCATGCTTTGCTGACAG 446  
DB 384 CACTTCTAGAG--GACACAGAGGAAGAGATGTAATCATGCTTTGCTGAGAG 440  
QY 447 ACCTTCCAGCATCAACAGAGCCGCTGAGATTCACCT--CTGTGAGAAATGCGCA 503  
DB 441 GCCTCTCCAGCATCAACAGAGCTGCTGATTTTCACTTCTCTCATGAGACMGCTG 500

QY 504 GTGGCATGAGGTCCGAGAGACCCTTATGTTCTTCTGTCAGTTCCTCCCAATGCCA 563  
DB 501 GTGACAGGAGGTCCGAGAGACCCTTATGTTCTTCTGTCAGTTCCTCCCAATGCCA 560  
QY 564 CCCAGCATGATATATAGAGTCTTGTGCTTAAGACCATATGACAGCAACCTCACTGA 623  
DB 561 CTTGACCTTTGAAGATGAGAGTCTTGTGCTTAAGACCATATGACAGCAACCTCACTGA 620  
QY 624 CAAGTCAGTACGTGTGAGAGAGATGACAGAGCTGAGTACCAAGCTTCTCTGAGAGCTG 683  
DB 621 CTACTCAGTACCTGCGAGAGAGTGTGAGAGCTGAGTACCAAGCTTCTCTGAGAGCTG 680  
QY 684 AAGCTCAAGCTCTGAG 743  
DB 681 AAGCTCAAGCTCTGAG 740  
QY 744 TGGCCACAGTCTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 803  
DB 741 TGGCCACAGTCTTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 800  
QY 804 TAAGGTTGAGGCAAGCATCGGCTGCGGAGGATGATGATGATGATGATGATGATGATGAT 863  
DB 801 TGAGAGTTGGGCAAGCATCGGCTGCGGAGGATGATGATGATGATGATGATGATGATGAT 860  
QY 864 GGATGTGCTGTCAGCAAGAGTTTGTGAGACTTCCGTGAGATTGCTGAGATGAGTGA 923  
DB 861 GGATGTGCTGTCAGCAAGAGTTTGTGAGACTTCCGTGAGATTGCTGAGATGAGTGA 920  
QY 924 TCATCAGCTTAAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 983  
DB 921 TCATCAGCTTAAGAGCTTATGATGATGATGATGATGATGATGATGATGATGATGATG 980  
QY 984 CAGGATGCTGTCAGCAAGAGTTTGTGAGACTTCCGTGAGATTGCTGAGATGAGTGA 1043  
DB 981 CAGGATGCTGTCAGCAAGAGTTTGTGAGACTTCCGTGAGATTGCTGAGATGAGTGA 1040  
QY 1044 ACGGATGCTGTCAGCAAGAGTTTGTGAGACTTCCGTGAGATTGCTGAGATGAGTGA 1103  
DB 1041 ACGGATGCTGTCAGCAAGAGTTTGTGAGACTTCCGTGAGATTGCTGAGATGAGTGA 1100  
QY 1104 TGTCTTCTCTTACTATGACAGAGGAGACAGCAATTTGCAAGAGGATATACATGATG 1163  
DB 1101 TGTCTTCTCTTACTATGACAGAGGAGACAGCAATTTGCAAGAGGATATACATGATG 1160  
QY 1164 TGTCTTCTCTTACTATGACAGAGGAGACAGCAATTTGCAAGAGGATATACATGATG 1223  
DB 1161 TGTCTTCTCTTACTATGACAGAGGAGACAGCAATTTGCAAGAGGATATACATGATG 1220  
QY 1224 G 1224  
DB 1221 G 1221

RESULT 4  
US-08-289-222E-2  
Sequence 2, Application US/08289222E  
Patent No. 6120760  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MARCELSTEIN, MURRAY & ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/289,222E

FILING DATE: 25-AUG-1999

CLASSIFICATION: 424

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US 08/289,222

FILING DATE: 12-AUG-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: DE P 44 23 190.3

FILING DATE: 07-JUL-1994

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: EPO 92102324.8

FILING DATE: 12-FEB-1992

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: PCT/EP93/00350

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: KITT'S, MONICA CHIN

REGISTRATION NUMBER: 36,105

REFERENCE/DOCKET NUMBER: P564-9021

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202/638-5000

TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 2272 base pairs

TYPE: nucleic acid

STRANDEDNESS: both

TOPOLOGY: Linear

MOLECULE TYPE: cDNA from mRNA

US-08-289-222E-2

Query Match 50.1%; Score 781; DB 3; Length 2272;

Best Local Similarity 79.9%; Pred. No. 3.4e-229;

Matches 959; Conservative 0; Mismatches 235; Indels 7; Gaps 3;

28 CACATTCCTCCAGGAGGCTGTCGTCAGAGCAGAGAGTTGA-AGCAGCTCCGTTGAGACC 86  
 24 CACACTTCTTCAGAGGCTCTGCGAGCAGAGCAGAGAGTTGAGAGCAGCAGCTGTTGAGACC 83  
 87 CTGAATATAGCCTTTCCTCTTAAAGAGGCTATCTCCAGCAATGAGCTCTCTCTGCG 146  
 84 CTGAGCCCTGAGTCTGTATTTGCTCAAGAAAGGCTCCCGCAGCAATGAGCTCTCATTTG 143  
 147 TCTGAGCT 206  
 144 TTTGAGCTTCT 203  
 207 GCCAGATGTTGGGCTGCAATCTTGAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGT 266  
 204 GTTCAGAGTGGGGGCGCCACTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 263  
 267 TGCCCAAGAAAGTATCCCTGAGCAAGCTGACCTGAGCCAGGCGCCCAATAGTACGAGG 326  
 264 TGGCCAAAGAAAGATCTTGGAGCAAGCTGACCTGAGCCAGGCGCCCAATAGTACGAGG 323  
 327 CAGTGTCCAGAGGAGGCTCTCAAGAGGCGCTGAGAGGCTCTGAGGAGGAGGAGGAGG 386  
 324 CTGTGTCCAGAGGAGGCTCTTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 383  
 387 CCGCTTGGAGCAGATGAGCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 446  
 384 CACTTCTAGAG--GAGCAAG 440  
 447 ACCGTCCAGATCAAGCAGAGCGGCTGAGTTCCACTT---CTGCTGAGATGAGAGCA 503  
 441 GCGTCTCCAGCATCAACGAGAGCTGCTTGTGATTTTTCACCTTCTCTCTGATAGAGAGCTG 500

504 GTGGCATGAGAGGTCGGGAGAGAGCCGCTTCATGTTCTTCGTGACAGTTCCCCCAATGCCA 563  
 501 GTGACAGGAGAGGTCGAG 560  
 564 CCCAGCATGATATATAGAGTTCTTGTGCTAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 623  
 561 CTTGAGAGCTTGAAG 620  
 624 CAGATCAGTACGAG 683  
 621 CTACTCAGTACGAG 680  
 684 AGCTCAG 743  
 681 AGCTCAG 740  
 744 TGGCCAG 803  
 741 TACCCAG 800  
 804 TAAAGGTTGAG 863  
 801 TGAGAGTTGGGGCAACACAGATTCACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860  
 864 GATGTGCTCTCAG 923  
 861 GATGTGCTCTCAG 920  
 924 TCATCCAG 983  
 921 TCATCCAG 980  
 984 CAGGATGAG 1043  
 981 CAGGATGAG 1040  
 1044 ACAGAGTGTGAG 1103  
 1041 ACAGAGTGTGAG 1100  
 1104 TGTCTTGTCTCTATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1163  
 1101 TGTCTTGTCTCTATATGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1160  
 1164 TGTCTGAG 1223  
 1161 TAGTAG 1220  
 1224 G 1224  
 1221 G 1221

RESULT 5  
 US-09-218-176-1  
 Sequence 1, Application US/09218176  
 Patent No. 6171584  
 GENERAL INFORMATION:  
 APPLICANT: H THEN, Gertrud  
 APPLICANT: NEIDHARDT, Helge  
 APPLICANT: BECHTOLD, Rolf  
 APPLICANT: POHL, Jens  
 APPLICANT: PAULISTA, Michael  
 TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
 TITLE OF INVENTION: TGF- FAMILY  
 NUMBER OF SEQUENCES: 49  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
 STREET: 655 Fifteenth Street, N. W., G Street Lobby,  
 STREET: Suite 330  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA

```

1 ZIP: 20005
2
3 COMPUTER READABLE FORM:
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5 MEDIUM TYPE: Floppy disk
6
7 COMPUTER: IBM PC compatible
8
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: Patent In Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/09/218,176
16
17 FILING DATE: Herewith
18
19 CLASSIFICATION:
20
21 PRIOR APPLICATION DATA:
22
23 APPLICATION NUMBER: 08/679, 048
24
25 FILING DATE: 12-JUL-1996
26
27 CLASSIFICATION:
28
29 PRIOR APPLICATION DATA:
30
31 APPLICATION NUMBER: PCT/EP96/03065
32
33 FILING DATE: 12-JUL-1996
34
35 PRIOR APPLICATION DATA:
36
37 APPLICATION NUMBER: PCT/EP93/00350
38
39 FILING DATE: 2-FEB-1993
40
41 PRIOR APPLICATION DATA:
42
43 APPLICATION NUMBER: US 08/482,577
44
45 FILING DATE: 7-JUN-1995
46
47 PRIOR APPLICATION DATA:
48
49 APPLICATION NUMBER: EP 92 102 324.8
50
51 FILING DATE: 12-FEB-1992
52
53 PRIOR APPLICATION DATA:
54
55 APPLICATION NUMBER: DE P 44 23 190.3
56
57 FILING DATE: 01-JUL-1994
58
59 PRIOR APPLICATION DATA:
60
61 APPLICATION NUMBER: DE 195 11 243.1
62
63 FILING DATE: 27-MAR-1995
64
65 ATTORNEY/AGENT INFORMATION:
66
67 NAME: KITTS, Monica Chln
68
69 REGISTRATION NUMBER: 36,105
70
71 REFERENCE/DOCKET NUMBER: P564-6010
72
73 TELECOMMUNICATION INFORMATION:
74
75 TELEPHONE: 202/638-5000
76
77 TELEFAX: 202/638-4810
78
79 INFORMATION FOR SEQ ID NO: 1:
80
81 SEQUENCE CHARACTERISTICS:
82
83 LENGTH: 2272 base pairs
84
85 TYPE: nucleic acid
86
87 STRANDEDNESS: single
88
89 TOPOLOGY: linear
90
91 MOLECULE TYPE: DNA
92
93 US-09-218-176-1

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[illegible]

Db	324	CTGTGTCAGAGCTGCTTTGAGGAGCTGCACCTGCACACCTCCACG66G6TCCCAAGAGGGG	383
Qy	387	CCCTGTTGGACATGACCAAGACAGAGATATGACATCATCAAGCTTTGCTGACACAG	446
Db	384	CACCTTCTAGAG--GACAAAGAGGAAACAGGATGTGAATCATCAGCTTGGCTGACACAG	440
Qy	447	ACCTCTCCAGATCAACACAGACCCGGCTCGAGTTCCAT---CTCTGGTACAAATGGCCA	503
Db	441	GCTCTTCACCATTAACCCAGACTGCTCTTGATTTTCACCTTCCTCTGTATTAAGACTGTG	500
Qy	504	GTCGACATGAGAGTCCGGACAGACCCGCTCATGTTCTTCTGTGAGATTCCGCCAATAGCA	563
Db	501	GTCAGAGGAGAGTCCAGACAGGCCAGTCTCATGTTCTTTGTGACGCTCCCTTCCAAATACA	560
Qy	564	CCGACACCATGAATATTAAGATCTTTGCTGTGAACACATATGACACCAACTCACCTTCA	623
Db	561	CTTGAGACCTTGAAGAGTGAAGTCTCTGTGGCTGGGTCACATATATCAACACTCACCTTGG	620
Qy	624	CAGATCAGTACGTGTGTCAGAGTGAATGACAGTGGCTGGTACAGCTTCCTCGGAGCTG	683
Db	621	CTACTCAGTACCTGCTGGAGGTGATGCCAATGGCTGGCATCACTCCCTTAGGGCTG	680
Qy	684	AAGCTCAAGCTGCTTGCAGACCAAGGACACTTACTCTGAGCTGGTACAGAAAGCCAG	743
Db	681	AAGCTCAAGCTGCTGTCAGGCGAGGCGACCTGACCTCTGAGCTGGTACTTGAGGCCAG	740
Qy	744	TGGCCCACTTCCTTATCTCTGGGCTGGTTTCCACAGGCCCTTTTGTGCAGCCACAG	803
Db	741	TACCCCAAGACTCAGTATCTCTGGGTGAGAGCTGCCATAGGCTTTTGTGGACGCCGG	800
Qy	804	TAAAGGTTTGAAGGCACATTCGGGTTGCGCGGAGAGATGATTTGCCAAGGGGGGTCCA	863
Db	801	TGAGAGTTGGGGGCAACACACAGATTCACCGACAGAGCATCGACTGGCCMAAGAGGTCCA	860
Qy	864	GGATGTGCTGTCGACAGAGATTTTGTAGACTTCCGAGATTTGGCTGGAATGACTGA	923
Db	861	GGATGTGCTGTCGACAGAGATTTTGTGACATTTCCGTGACATTTGCTGGCAGCATGGA	920
Qy	924	TCAATCAGCCGTGAAGGCTATGCCATGAATCTTGCACACTGGGCACTGGCCATACATATGG	983
Db	921	TCATTCAGCTGAGGGGTAGGCCATGAACCTTCTCATATAGGCAATGGCCATACACATAG	980
Qy	984	CAGGCAATGCTGGCATCTCTGCTCCTTTCACACTGCAGTGCATGTAATCTGCTCAAAGCA	1043
Db	981	CAGGCAATGCTGCTATTTGCTGCTCCTTTCACACTGCAGTGCATGTAATCTTTCAAAGCA	1040
Qy	1044	ACGCACTGCTGGCACCACCTGCGAGGGGCTCTGCTGCTGCTGCTCAATCTTCGGCCCTC	1103
Db	1041	ACACACCTTCAAGCCACACACTGCGAGGGGCTCAATGCTGTACCCACGCGCCGCCCC	1100
Qy	1104	TGCTTTGCTCTTATATGACAGGACAGCAACATTTGCAAGAGCGGATATATCTTACATGG	1163
Db	1101	TGCTCTGCTCTATATATGACAGGGAAGCAACATTTGCAAGAGCTGATCTGACATCG	1160
Qy	1164	TGCTGAGGCTTCGGGCTGATTTACCTTTGGGTATACAGGCTGGCTGACGTAGATG	1223
Db	1161	TGATGAGGCTCTGGGCTCAGTTACTATGTGTGTATGAGGACGCCAAAGTTGCATG	1220
Qy	1224	G	
Db	1221	G	

RESULT 6  
 US-09-054-526B-2  
 : Sequence 2, Application US/09054526B-2  
 : Patent No. 6,197,550.  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: H TTEK, GERTROD  
 : APPLICANT: NEIDHARDT, HELGE  
 : APPLICANT: BECHTOLD, ROLEF  
 : APPLICANT: POHL, JENS



TITLE OF INVENTION: FAMILY  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM  
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
STREET: SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/289, 222E  
FILING DATE: 25-AUG-1999  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289, 222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-9021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA from mRNA  
US-08-289-222E-5

Query Match 13.6% Score 212.2; DB 3; Length 265;  
Best Local Similarity 87.5% Pred. No. 1.7e-55;  
Matches 232; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 925 CATCCAGCCTGAAGCCTATGCACTTCTGCACTGGGCGAGTGGCCACTACATGTCGC 984  
DB 1 CATCCAGCCTGAAGCCTATGCACTTCTGCACTGGGCGAGTGGCCACTACATGTCGC 60  
QY 985 AGGCATGCTGCGATCTGCTGCTCTTTCACACTGAGTGTGATGCTGCAAGCCAA 1044  
DB 61 AGGCATGCTGCGATCTGCTGCTCTTTCACACTGAGTGTGATGCTGCAAGCCAA 120  
QY 1045 CCAGCTGCTGAGCAGTGGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104  
DB 121 CACAGCTGAGCAGCAGTGGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
QY 1105 GTCTTGTCTACTATGACAGGAGCAACATTTGCAAGAGGATATACCTGACATGCT 1164  
DB 181 GTCTTGTCTACTATGACAGGAGCAACATTTGCAAGAGGATATACCTGACATGCT 240  
QY 1165 GGTGAGGCTGCGGGGTGATGTTAG 1189  
DB 241 AGTAGAGGCTGTGGTGCAGTTAG 265  
RESULT 8

US-09-054-526B-5  
Sequence 5, Application US/09054526B  
Patent No. 6197550  
GENERAL INFORMATION:  
APPLICANT: H TTEEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
STREET: SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054, 526B  
FILING DATE: 03-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289, 222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-8005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 265 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA from mRNA  
US-09-054-526B-5

Query Match 13.6% Score 212.2; DB 4; Length 265;  
Best Local Similarity 87.5% Pred. No. 1.7e-55;  
Matches 232; Conservative 0; Mismatches 33; Indels 0; Gaps 0;  
QY 925 CATCCAGCCTGAAGCCTATGCACTTCTGCACTGGGCGAGTGGCCACTACATGTCGC 984  
DB 1 CATCCAGCCTGAAGCCTATGCACTTCTGCACTGGGCGAGTGGCCACTACATGTCGC 60  
QY 985 AGGCATGCTGCGATCTGCTGCTCTTTCACACTGAGTGTGATGCTGCAAGCCAA 1044  
DB 61 AGGCATGCTGCGATCTGCTGCTCTTTCACACTGAGTGTGATGCTGCAAGCCAA 120  
QY 1045 CCAGCTGCTGAGCAGTGGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1104  
DB 121 CACAGCTGAGCAGCAGTGGGCGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
QY 1105 GTCTTGTCTACTATGACAGGAGCAACATTTGCAAGAGGATATACCTGACATGCT 1164  
DB 181 GTCTTGTCTACTATGACAGGAGCAACATTTGCAAGAGGATATACCTGACATGCT 240



Db 181 GTCCTCGCTATTATGACAGGCGACACCAATTTOTCAAGACTGACATACCTGACATGCT 240

QY 1165 GGTGAGGCGCTGCGGGGTGTAGTTAG 1189

Db 241 AGTAGAGGCTGTGGGTGCAGTTAG 265

## RESULT 9

```

US-08-455-550-2
: Sequence 2, Application US/08455550
: Patent No. 5670338
: GENERAL INFORMATION:
: APPLICANT: MURAKAMI, KAZUO
: APPLICANT: UENO, NAOTO
: APPLICANT: KATO, YUKIO
: TITLE OF INVENTION: XENOPUS LAEVIS BONE MORPHOGENETIC PROTEINS AND USE THEREOF
: NUMBER OF SEQUENCES: 22
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dike, Bronstein, Roberts & Cushman
: STREET: 130 Water Street
: CITY: Boston
: STATE: MA
: COUNTRY: USA
: ZIP: 02109
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq Version 1.5
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/455,550
: FILING DATE: 31-MAY-1995
: CLASSIFICATION: 514
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/056,564
: FILING DATE: 30-APR-1993
: APPLICATION NUMBER: 07/577,892
: FILING DATE: 05-SEP-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Eisenstein, Ronald I
: REGISTRATION NUMBER: 30628
: REFERENCE/DOCKET NUMBER: 40302-FWC-DIV
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 617-523-3400
: TELEFAX: 617-523-6440
: TELEX: 200291
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 687 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: FRAGMENT TYPE:
: ORIGINAL SOURCE:
: US-08-455-550-2

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	Query Match	Similarity	9.2%	Score 143.4	DB 1	Length 687
Matches	266	Conservative	61.7%	Pred. No. 3.3e-34	0	Mismatches 156; Indels 9; Gaps 2
QY	775	TTTCCACAGCCCTTTTGGGACGCCAGGTTAAGGGT	--TGAGGGCAAGCATCGGGTTCCG	831		
DB	67	TTTCCACAGCCATTTTGGTAGCACAGGCCAAAGTCCATGAAACAAGTCACCATGCTAC	126			
QY	832	CGCGCGAGTATCATTTGCCAAGCGGGGTCACAGATGCTGTCCGACAAAGATTTTTTGT	891			
DB	127	AAAGAGAAAGTCTTAAGCTGTGATCAGAAATCCATCTGCTGTGAGAAAGATTATTATGT	186			
QY	892	AGACTTCCGTCAGATTGGCTGGAAATGACTGATCATCCACCCCTAAGCGCTATCCATGAA	951			

Db	187	ACAGCTTCAGAGATATTGGGTGCAANTGATTGATTTATATAAACAGAGGATATTCAGATATAA	246
Qy	952	CTTCTGCACTGGGGCAGTGGCCCACTACATGTGCGAGCGATGCGTGGCATCTTCTGCTCCTT	1011
Db	247	TATATGTCATGGGCGCTTGGGCCCAATGCATATCCCTGCGAGCCCGAGGTACGGAGAGCTCATTT	306
Qy	1012	TACACTGCAGTGTGTAATCTGCTCAAAAGCCAAACGCACTGTGGCACACACTGGCAGGGG	1071
Db	307	CCACACACAGGATTTAAATCTCATTTAAGGCCAAC-----AATATCCAGACACGACAGTGA	360
Qy	1072	CTCGTGTCTGCGTCCCTACATCTGGGGCCCTCTGTCTTTGCTCTACATATGACAGGAGAC	1133
Db	361	CTCATGTCTGTGCCCTACCCAAAAGGGGCCCTTGTTCATGCTTTTACTTTGTATACAAATAA	420
Qy	1132	CAACATGTGCAGAGGAGATATACCTGCATGCTGTGCGAGAGCCGCGGGGTAGTTACTT	1191
Db	421	CAACGTTCTTCAGACATGCATTTGCCGATATGATTGTGGAACCGTGTGGGTGTACCTAGG	480
Qy	1192	TATGGGTGATA 1202	
Db	481	CTTGGGCTTACA 491	

## RESULT 10

US-08-765-662-13  
Sequence 13, Application us/08765662  
Patent No. 5929213  
GENERAL INFORMATION:  
APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/765,662  
FILING DATE: 28-APR-1997  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745  
FILING DATE: 12-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Halle, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/042W01 (FD-3830)  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2419, base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 218...1267  
OTHER INFORMATION:





STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: Windows95  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/184,933  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/274,215  
FILING DATE: 13-JUL-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/040001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-68-5099  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...357  
US-09-184-933-11

Query Match  
Best Local Similarity 62.8%; Score 136; DB 3; Length 360;  
Matches 230; Conservative 0; Mismatches 130; Indels 6; Gaps 1;

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DB 1 CGGGCCAG 60  
QY 884 TTTTGTGACCTCCGTGAGATGCGTGAATGATGATGATGATGATGATGATGAT 943  
DB 61 CATTAAGTACCTCCGTGAGATGCGTGAATGATGATGATGATGATGATGATGAT 120  
QY 944 GCCATGAATCTGACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003  
DB 121 CAGCTGAATCTGACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
QY 1004 GCGTCTTTACACATGCTGATGATGATGATGATGATGATGATGATGATGAT 1063  
DB 181 GCGTCTTTACACATGCTGATGATGATGATGATGATGATGATGATGATGAT 234  
QY 1064 GCGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123  
DB 235 GCGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 294  
QY 1124 AGGACAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
DB 295 CATTAAGTACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 354  
QY 1184 AGTAG 1189  
DB 355 AGTAG 360

RESULT 15  
PCT-US95-08745-11  
; Sequence 11. Application PC/TUS9508745  
; GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08745  
FILING DATE: 12-JUL-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Hallie, Ph.D., Lisa A.  
REGISTRATION NUMBER: 38,347  
REFERENCE/DOCKET NUMBER: 07265/042M01 (FD-3830)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 619-678-5070  
TELEFAX: 619-678-5099  
TELEX:  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 1...357  
OTHER INFORMATION:  
PCT-US95-08745-11

Query Match  
Best Local Similarity 62.8%; Score 136; DB 5; Length 360;  
Matches 230; Conservative 0; Mismatches 130; Indels 6; Gaps 1;

QY 824 CGGTTCCGCCGCGAGGATGATGCGAGGGGGGTCAGAGATGCTGTCGACAGAG 883  
DB 1 CGGGCCAG 60  
QY 884 TTTTGTGACCTCCGTGAGATGCGTGAATGATGATGATGATGATGATGATGAT 943  
DB 61 CATTAAGTACCTCCGTGAGATGCGTGAATGATGATGATGATGATGATGATGAT 120  
QY 944 GCCATGAATCTGACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1003  
DB 121 CAGCTGAATCTGACAGTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180  
QY 1004 GCGTCTTTACACATGCTGATGATGATGATGATGATGATGATGATGATGAT 1063  
DB 181 GCGTCTTTACACATGCTGATGATGATGATGATGATGATGATGATGATGAT 234  
QY 1064 GCGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1123  
DB 235 GCGAGTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 294  
QY 1124 AGGACAGCAATGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1183  
DB 295 CATTAAGTACCTGCTGATGATGATGATGATGATGATGATGATGATGATGAT 354  
QY 1184 AGTAG 1189

Tue Oct 15 13:49:42 2002

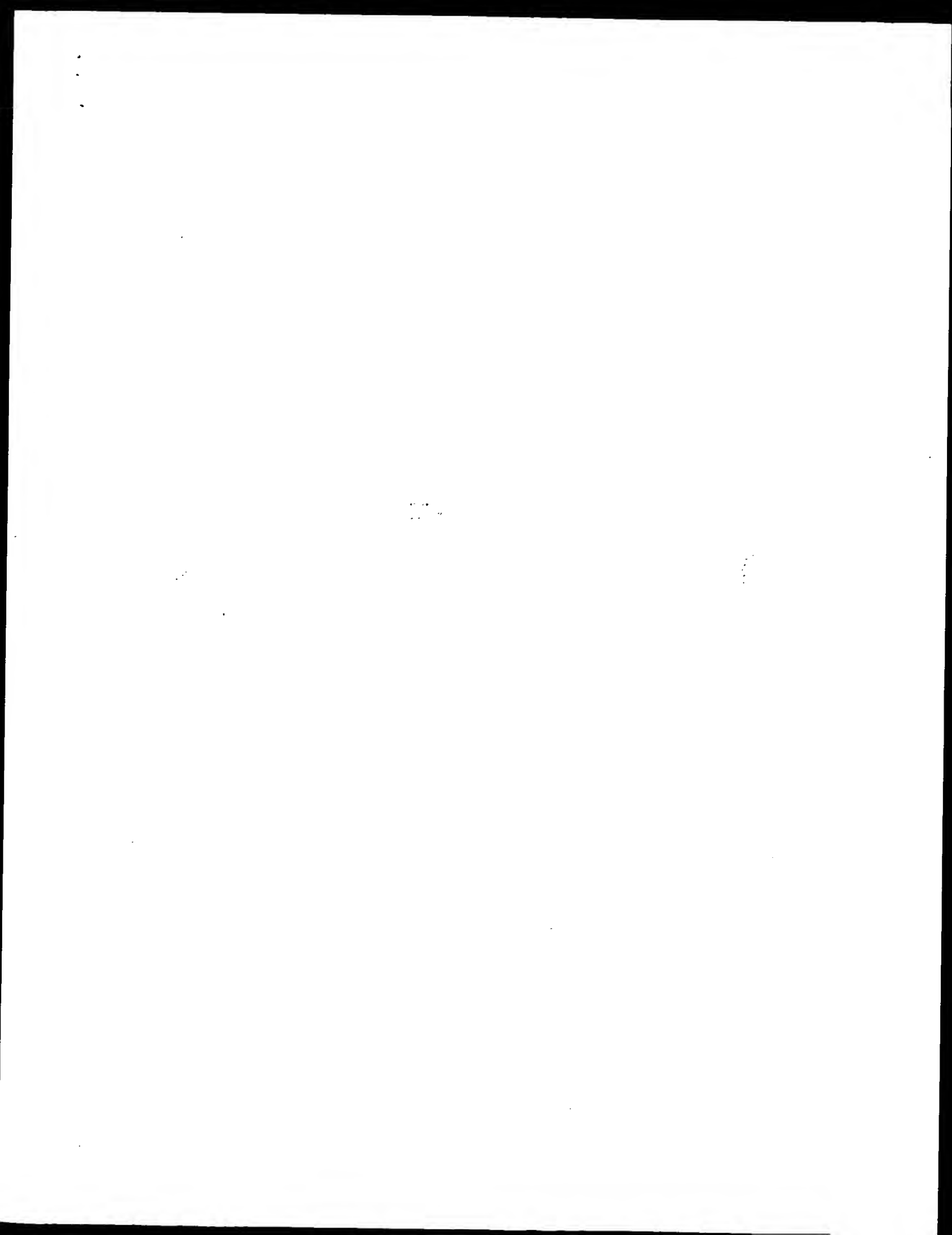
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Page 13

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Db 355 AGCTAG 360

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Job time : 47.2042 secs

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 11, 2002, 22:15:08 ; Search time 1258.6 seconds  
(without alignments)  
16707.608 Million cell updates/sec

Title: US-09-684-383-3  
Perfect score: 1558  
Sequence: 1 AACGAGTCATGCGCAGTCGGA.....ATGCTTAGTGTCTCCCTT 1558

Scoring table: IDENTITY-NUC  
Gapop 10.0, Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues  
Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: EST:  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estlm:\*  
4: em\_estlm:\*  
5: em\_estlm:\*  
6: em\_estlm:\*  
7: em\_estlm:\*  
8: em\_estlm:\*  
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13: em\_estlm:\*  
14: em\_estlm:\*  
15: em\_estlm:\*  
16: em\_estlm:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	726.6	46.6	829	10	B1329959 602980519
3	716.8	46.0	893	10	B1246740 602959660
4	716.8	46.0	893	10	B1246740 602959660
5	706.6	45.4	841	10	B1145698 602909844
6	696.6	44.7	758	10	B1328115 602979264
7	653.8	42.0	823	10	B1328115 602979264
8	643.6	41.3	975	10	B1328115 602979264
9	509	32.7	636	10	B1328115 602979264
10	413.2	26.5	1011	11	BC020693 Homo sap1
11	299.6	19.2	493	9	AA237913 mx14e05.r
12	261.2	16.8	312	9	AI287120 u171g11.y
13	252	16.2	541	10	B1328115 602979264
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17	127.2	8.2	714	10	B1152811 602917943

18	119	7.6	367	10	BG713244
19	116.4	7.5	546	10	BF061329
20	116.4	7.5	535	10	BF083319
21	116.4	7.5	627	9	AI800922
22	116.4	7.5	634	10	BF000451
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24	115.2	7.4	558	10	AI433268
25	114.8	7.4	558	10	BE506007
26	114.6	7.4	504	10	BM219131
27	114.6	7.4	536	10	BF508647
28	112.2	7.2	493	9	AI753619
29	111	7.1	667	10	B1696144
30	110.2	7.1	982	10	BF689098
31	109.4	7.0	516	9	AI157212
32	107.8	6.9	372	10	BF542340
33	107.8	6.9	389	9	AM385664
34	104.8	6.7	535	9	AI157878
35	103.2	6.6	942	10	BF309695
36	101.8	6.5	661	9	BB667192
37	101.4	6.5	401	10	BG995292
38	99.8	6.4	831	12	CNS02TIT
39	99	6.4	920	12	CNS03ELX
40	98.8	6.3	669	10	B1646826
41	98.4	6.3	515	9	AA587288
42	98.4	6.3	493	10	BF000351
43	95.8	6.1	623	9	AW911189
44	94.4	6.1	368	10	B1961659
45	94.4	6.1	401	10	B1960944

## ALIGNMENTS

RESULT 1  
LOCUS B1148079  
DEFINITION 602912428P1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5053471 5',  
mRNA sequence.  
ACCESSION B1148079  
VERSION B1148079.1 GI:14608080  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus.  
REFERENCE 1 (bases 1 to 941)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: cgaabs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L14M1145 row: 9 column: 08  
High quality sequence stop: 887.  
Location/Qualifiers  
1. '941  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
/clone\_lib="NCI\_CGAP\_L19"  
/lab\_host="DH10B (T1 phage-resistant)"  
/note="Organ: liver; Vector: pCMV-SPORT6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 Kb. Constructed by Life Technologies. Note: this is a NCI\_CGAP library."

BASE COUNT

202 a 260 c 246 g 233 t



## ORIGIN

Query Match 48.3%; Score 752.2; DB 10; Length 941;  
 Best Local Similarity 95.1%; Pred. No. 6.2e-199;  
 Matches 874; Conservative 0; Mismatches 33; Indels 12; Gaps 9;

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OY 650 GCCAGTGGCTGTCACCAAGCTCTCTGGG-ACCTGAAGCTCAAGCTGCTGACGACGG 708
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DB 1 GCCAGTGGCTGTCACCAAGCTCTCTGGG-ACCTGAAGCTCAAGCTGCTGACGACGG 59
OY 709 ACACCTTACTCTGTGAGCTGTACCAAGAAAGCAGGTGAGCCACAGTCTCTGATCTCTGG 768
    |||||||
DB 60 ACACCTTACTCTGTGAGCTGTACCAAGAAAGCAGGTGAGCCACAGTCTCTGATCTCTGG 119
OY 769 CTGCTTTTCCACAGAGGCTTTTGTGCGACCCAGGTAAGGCTTGAAGGCAAGCATCGGCT 828
    |||||||
DB 120 CTGCTTTTCCACAGAGGCTTTTGTGCGACCCAGGTAAGGCTTGAAGGCAAGCATCGGCT 179
OY 829 TCCGCGGCGAGTATCATTCAGGCGGCGGTCGACAGTGCCTCTGACAAAGATTTT 888
    |||||||
DB 180 TCCGCGGCGAGTATCATTCAGGCGGTCGACAGTGCCTCTGACAAAGATTTT 238
OY 889 TGTAGACTTCCTGAGATGCTGCTGCAATGACTGATCATCCAGCTGAAGCTATGCCAT 948
    |||||||
DB 239 CGTAGACTTCCTGAGATGCTGCTGCAATGACTGATCATCCAGCTGAAGCTATGCCAT 298
OY 949 GAACCTTCTGAGCTGGGAGTGGCCACTACATGTGCGAGGCAATGCTGCTGCTGCTC 1008
    |||||||
DB 299 GAACCTTCTGAGCTGGGAGTGGCCACTACATGTGCGAGGCAATGCTGCTGCTGCTC 358
OY 1009 CTTTCACACTGCACTGCTGCAATGCTGCAAGGCAAGGCAAGCTGCTGCTGCTGCTG 1068
    |||||||
DB 359 CTTTCACACTGCACTGCTGCAATGCTGCAAGGCAAGGCAAGCTGCTGCTGCTGCTG 418
OY 1069 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1128
    |||||||
DB 419 GGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 478
OY 1129 GAGCAACATTTGTCACAGGATATACCTGATGTGCTGAGGCTGCGGGTGTACTTA 1188
    |||||||
DB 479 GAGCAACATTTGTCACAGGATATACCTGATGTGCTGAGGCTGCGGGTGTACTTA 538
OY 1189 GCTTATGCTGATACAGGCTGCTGAGTATGAGTATGCTGCTGCTGCTGCTGCTG 1247
    |||||||
DB 539 GCTTATGCTGATACAGGCTGCTGAGTATGAGTATGCTGCTGCTGCTGCTGCTG 598
OY 1248 GTTCCACACTTCTGCTGAGATGAAACACCTTTCTAAGCATGAGCATCCCTCTGTGA 1307
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DB 599 GTTCCACACTTCTGCTGAGATGAAACACCTTTCTAAGCATGAGCATCCCTCTGTGA 658
OY 1308 CTTGAGGGATGCACTCTTAAGAGAGTCACTAGTACCAACAGCCTTTCTCTCTGG 1367
    |||||||
DB 659 CTTGAGGGATGCACTCTTAAGAGAGTCACTAGTACCAACAGCCTTTCTCTCTGG 718
OY 1368 GACATGCTGAGCAGTACACCATCCCTGAGCTTAAGTAAAGGCTTAATGCA---CTC 1423
    |||||||
DB 719 GACATGCTGAGCAGTACACCATCCCTGAGCTTAAGTAAAGGCTTAATGCA---CTC 778
OY 1424 CTACATATATATGCTATTTTCTAGCAAAACACCCCTAG-CTCCCTTAGTCAACTA- 1481
    |||||||
DB 779 CCACAAAGATGCTATTTTCTAGCAAAACACCCCTAG-CTCCCTTAGTCAACTA- 838
OY 1482 TGTATATCTACTCTGCTCTCC-TCACCTTGCACCGGAGAGCTCTTAATTC-ACGATGAT 1539
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DB 839 TGTATATCTACTCTGCTCTCC-TCACCTTGCACCGGAGAGCTCTTAATTC-ACGATGAT 898
OY 1540 TGCCTAGTCTCTCTCT 1558
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DB 899 TGCCTAGTCTCTCTCT 917
  
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RESULT 2  
 B1329959

LOCUS B1329959 829 bp mRNA linear EST 30-JUL-2001  
 DEFINITION 602980519F1 NCL\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5133317 5',  
 mRNA sequence.  
 ACCESSION B1329959  
 VERSION B1329959.1 GI:15014616  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 829)  
 NIH-MGC <http://mgc.nhl.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 CONTACT: Robert Strausberg, Ph.D.  
 Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
 Plate: LLM11327 row: f column: 06  
 High quality sequence stop: 789.  
 Location/Qualifiers  
 1..829  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5133317"  
 /clone\_id="NCL\_CGAP\_L19"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: liver; Vector: pCMV-Sport6; Site-1: NCI;  
 Site-2: Salt; Cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCL\_CGAP Library."  
 BASE COUNT 187 a 246 c 217 g 179 t  
 ORIGIN

Query Match 46.6%; Score 726.6; DB 10; Length 829;  
 Best Local Similarity 97.5%; Pred. No. 8.1e-192;  
 Matches 791; Conservative 0; Mismatches 14; Indels 6; Gaps 5;

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OY 1 AAGGATCATGCGACGAGGTCAGTCACTTCTCCAGGCTGCTGCTGCTGCTGCTGCTG 60
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DB 22 AAGGATCATGCGACGAGGTCAGTCACTTCTCCAGGCTGCTGCTGCTGCTGCTGCTG 81
OY 61 AAGATTAAG-CACCTCCGTTGAGACCCCTGAATATAGCTTTGGGTCCTTTAAGGAGGT 119
    |||||||
DB 82 AAGATTAAGCACCTCCGTTGAGACCCCTGAATATAGCTTTGGGTCCTTTAAGGAGGT 141
OY 120 ATTCCTCAGCAATGAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 179
    |||||||
DB 142 ATTCCTCAGCAATGAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 201
OY 180 TAGTGAACCCCAAACTAGAGGTCATGAGGTCATGAGGTCATGAGGTCATGAGGTCAT 239
    |||||||
DB 202 TAGTGAACCCCAAACTAGAGGTCATGAGGTCATGAGGTCATGAGGTCATGAGGTCAT 261
OY 240 AGAGCCAGCGGAGCTGCTCTGATTTGGCCAAAGAAAGTATCTGGAAGCAAGCTGACAC 299
    |||||||
DB 262 AGAGCCAGCGGAGCTGCTCTGATTTGGCCAAAGAAAGTATCTGGAAGCAAGCTGACAC 321
OY 300 TCAGCCAGCGGCGCATACATGAGTGGCCAGTGCAGAGGAGGCTCTCAAGACCGGCTGC 359
    |||||||
DB 322 TCAGCCAGCGGCGCATACATGAGTGGCCAGTGCAGAGGAGGCTCTCAAGACCGGCTGC 381
OY 360 AGGCTCTCGGCGGCTGTCAGAGGAAACCTGTTGAGCATGAGCAGAGAGAAAGAT 419
    |||||||
DB 382 AGGCTCTCGGCGGCTGTCAGAGGAAACCTGTTGAGCATGAGCAGAGAGAAAGAT 441
OY 420 ATGAGATCATCAGCTTTTGTCAGACAGACCTCTCCAGATCAACGACGCGGCTGAGT 479
  
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DB 442 ATGAGATCATCAGCTTCTGACACAGACCTCTCCAGCATCAACAGACCCGGCTCGAGT 501  
 OY 480 TCCACTCTCTGAGTATGGCAGTGGCATGGGTCCGGCAGACCCGGCTCTATGTTCT 539  
 DB 502 TCCACTCTCTGAGTATGGCAGTGGCATGGGTCCGGCAGACCCGGCTCTATGTTCT 561  
 OY 540 TCCGTCAGTTCCTCCACATGTCACCATGATATATAGATTCTTGTCTAGAC 599  
 DB 562 TCCGTCAGTTCCTCCACATGTCACCATGATATATAGATTCTTGTCTAGAC 621  
 OY 600 CATATGACACCACTTACCTTACAGAGTACAGTGTGTGAGTGAATGCCAGTGTCT 659  
 DB 622 CATATGACACCACTTACCTTACAGAGTACAGTGTGTGAGTGAATGCCAGTGTCT 679  
 OY 660 GGTACGACCTTCTCTGAGCAGTGAAGTCTTGTGACCCAGCAGACCTTACTC 719  
 DB 680 GGTACGACCTTCTCTGAGCAGTGAAGTCTTGTGACCCAGCAGACCTTACTC 739  
 OY 720 TGGAGCTGTGACCAAGAGTGGCCACAGTCTTGTGATCTTGTGCTTGTCTTCC 779  
 DB 740 TGGAGCTGTGACCAAGAGTGGCCACAGTCTTGTGATCTTGTGCTTGTCTTCC 797  
 OY 780 ACAGGCTTGTGACCAAGAGTGGCCACAGTCTTGTGATCTTGTGCTTGTCTTCC 810  
 DB 798 ACAGGCTTGTGACCAAGAGTGGCCACAGTCTTGTGATCTTGTGCTTGTCTTCC 827

RESULT 3  
 B1246740 893 bp mRNA linear EST 17-JUL-2001  
 LOCUS B1246740  
 DEFINITION 60299984F1 NCL\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5125287 5',  
 mRNA sequence.

ACCESSION B1246740 GI:14790995  
 VERSION B1246740.1  
 KEYWORDS EST.

SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS NIH-MGC http://mgc.ncl.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strusberg, Ph.D.  
 Email: g9abs-remail.nih.gov  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 cDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LLM11306 row: 9 column: 16  
 High quality sequence stop: 778.

FEATURES  
 SOURCE location/qualifiers

1..893  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5125287"  
 /clone\_lib="NCL\_CGAP\_L19"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: liver; Vector: PCMV-SPORT6; Site: 1; NotI:  
 Site: 2; SalI: cloned unidirectionally. Primer: Oligo dt.  
 Average insert size 1.9 kb. Constructed by Life  
 Technologies. Note: this is a NCL\_CGAP Library."  
 BASE COUNT 196 a 259 c 242 g 196 t

Query Match 46.0%; Score 716.8; DB 10; Length 893;  
 Best Local Similarity 96.0%; Pred No. 4.6e-189;  
 Matches 854; Conservative 0; Mismatches 22; Indels 14; Gaps 11;

OY 95 AGCTTTGGGCTCTTAAAGAGGCTATCCCTCAGCAATGAGCTCTCTTGGCTTGGCT 154  
 DB 1 AGCTTTGGGCTCTTAAAGAGGCTATCCCTCAGCAATGAGCTCTCTTGGCTTGGCT 60  
 OY 155 CTTCCTGCTCTGACTCCAGCAGTACTGAAACCCAAACTAGAGGCTCATGCCAGCA 214  
 DB 61 CTTCCTGCTCTGACTCCAGCAGTACTGAAACCCAAACTAGAGGCTCATGCCAGCA 120  
 OY 215 TGTGGGGTCCCATCTTTGACCTGAGAGCCAGCGGAGCTCTTCTGATTTGGCCAG 274  
 DB 121 TGTGGGGTCCCATCTTTGACCTGAGAGCCAGCGGAGCTCTTCTGATTTGGCCAG 180  
 OY 275 AAAAGTATCTTGAGCAAGCTGACCTGAGCCAGCGGCTCATCTAGTGGGCAAGTCC 334  
 DB 181 AAAAGTATCTTGAGCAAGCTGACCTGAGCCAGCGGCTCATCTAGTGGGCAAGTCC 240  
 OY 335 AGAGGGCTCTCAAGAGCGGCTGAGCGGCTCCGGGGCTGAGAGGGAACCTGTTC 394  
 DB 241 AGAGGGCTCTCAAGAGCGGCTGAGCGGCTCCGGGGCTGAGAGGGAACCTGTTC 300  
 OY 395 GAGCATGACCAAGACAAAGAAATATGATCATCAGCTTTGTGACACAGACTCTCC 454  
 DB 301 GAGCATGACCAAGACAAAGAAATATGATCATCAGCTTTGTGACACAGACTCTCC 360  
 OY 455 AGCATCAACAGACCGGCTGAGCTTCTGCTGAGTGA-ATGGCAGTGGCATGGA 513  
 DB 361 AGCATCAACAGACCGGCTGAGCTTCTGCTGAGTGA-ATGGCAGTGGCATGGA 420  
 OY 514 GGTCCGACACACCGGCTTCTGCTGAGTGGTCCCAATGCAACCAAGCAT 573  
 DB 421 GGTCCGACACACCGGCTTCTGCTGAGTGGTCCCAATGCAACCAAGCAT 480  
 OY 574 GAATATAGAGTCTTGTGCTGAGTGGTCCCAATGCAACCAAGCAT 633  
 DB 481 GAATATAGAGTCTTGTGCTGAGTGGTCCCAATGCAACCAAGCAT 540  
 OY 634 CGTGG-TGCAGTGAATGCCAGTGGCTGTACACCTTCTCTGAGCCTGAAGCTCAAG 692  
 DB 541 CGTGGTGCAGTGAATGCCAGTGGCTGTACACCTTCTCTGAGCCTGAAGCTCAAG 600  
 OY 693 CTGCTTCACACCGGACGACCTTACTCTGG-AGCTGTACAGAAAGCAGGTGGCCCA- 750  
 DB 601 CTGCTTCACACCGGACGACCTTACTCTGGAAAGCTGTGTACAGAAAGCAGGTGGCCCA 660  
 OY 751 CAATTCTTATCTCTGGGCTGTTTCCACAGGCTTTTGTGGCAGCCAGGTAAGGT 810  
 DB 661 CAATTCTTATCTCTGGGCTGTTTCCACAGGCTTTTGTGGCAGCCAGGTAAGGT 720  
 OY 811 T--GAGGGCAAGCATC--GGGTTCCGGGCGAGGTATCG-ATTGGCAGGGGGGTCCAG 864  
 DB 721 TTGAGGGGCAAGCATCGGGGTTCCGGGCGAGGTATCGATTGGCAGGGGGGTCCAG 780  
 OY 865 GA-TGTCTCTGACAGAGTCTTTTGTAGACTCTCGTGAAGTGGCTGAATGAC-TGG 922  
 DB 781 GATTGTCTCTGACAGAGTCTTGTAGAACTCTCGTGAATGCTTGGCTGAATGAC-TGG 840  
 OY 923 ATCAATCAGCTGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 972  
 DB 841 ATCAATCAGCTGAGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 888

RESULT 4  
 B1145698 841 bp mRNA linear EST 05-JUL-2001  
 LOCUS B1145698  
 DEFINITION 60299984F1 NCL\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5050810 5',  
 mRNA sequence.  
 ACCESSION B1145698  
 VERSION B1145698.1 GI:14605699  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 841)  
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L1M1138 row: h column: 11  
 High quality sequence stop: 835.  
 Location/Qualifiers

FEATURES  
 Source 1..841  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5050810"  
 /clone\_lib="NCI CGAP\_L19"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: Liver; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 181 a 238 c 221 g 201 t

Query Match 45.8%; Score 714; DB 10; Length 841;  
 Best Local Similarity 97.1%; Pred. No. 2.7e-188;  
 Matches 812; Conservative 0; Mismatches 15; Indels 9; Gaps 8;

OY 678 GACCTAAGCTCAAGCTGCTTGCAGCCAGGACACCTTACTGTGAGCTGTACAGAAA 737  
 DB 1 GACCTAAGCTCAAGCTGCTTGCAGCCAGGACACCTTACTGTGAGCTGTACAGAAA 59  
 OY 738 GCCAGTGGCCACAGTTCCTGATCTGGGCTGGTTCCACAGGCTTTTGTGGCAG 797  
 DB 60 GCCAGTGGCCACAGTTCCTGATCTGGGCTGGTTCCACAGGCTTTTGTGGCAG 119  
 OY 798 CCCAGTAAGGCTTGAAGGAGCAGATCGGTTCCGCGGAGATTCGATTCGACAGGGG 857  
 DB 120 CCCAGTAAGGCTTGAAGGAGCAGATCGGTTCCGCGGAGATTCGATTCGACAGGGG 179  
 OY 858 GGTCCAGATGTCTGTGCAACAGATTTTGTAGACTTCCTGATGATGGCTGCAATG 917  
 DB 180 GGTCCAGATGTCTGTGCAACAGATTTTGTAGACTTCCTGATGATGGCTGCAATG 239  
 OY 918 ACTGATCATCCAGCTGGAAGGCTATGCCATGAACCTTGTGCACTGGCAGTCCCACTAC 977  
 DB 240 ACTGATCATCCAGCTGGAAGGCTATGCCATGAACCTTGTGCACTGGCAGTCCCACTAC 299  
 OY 978 ATGTGACAGGACGCGGATCTGCTGCTTTCACACGTCATGCTGATTCGCTCA 1037  
 DB 300 ATGTGACAGGACGCGGATCTGCTGCTTTCACACGTCATGCTGATTCGCTCA 359  
 OY 1038 AAGCCAAACGCTGCTGACACCATGCGAGGGCTGCTGCTGCTTACATCTCGGC 1097  
 DB 360 AAGCCAAACGCTGCTGACACCATGCGAGGGCTGCTGCTGCTTACATCTCGGC 419  
 OY 1098 GCCCTCTGTTTCTTACTATGACAGGACACCAACATTTGTCAAGAGGATATACCTG 1157  
 DB 420 GCCCTCTGTTTCTTACTATGACAGGACACCAACATTTGTCAAGAGGATATACCTG 479  
 OY 1158 ACATGCTGTGAGGCTGGGGGTGTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 1217  
 DB 480 ACATGCTGTGAGGCTGGGGGTGTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAGTTAG 539  
 OY 1218 AGAATGGCTTCTCTCAGGAA-GGGAAACTCTGTTCCCACTTGTGCAAGATGGAACAC 1276  
 DB 1218 AGAATGGCTTCTCTCAGGAA-GGGAAACTCTGTTCCCACTTGTGCAAGATGGAACAC 1276

DB 540 AGAATGGCTTCTCTCAGGAAAGGGAACACTGTTCACACTTCTGTCCAGATGGAACAC 599  
 OY 1277 CTTTCTAAGCATGACAGACATCCCTGTGTGAGCTTACAGGGATCCACCTTAAG-AGAGACT 1335  
 DB 600 CTTTCTAAGCATGACAGACATCCCTGTGTGAGCTTACAGGGATCCACCTTAAGAGAGACT 659  
 OY 1336 CACTGTGACCAACAGGCTTCTCTCTCCGAGACAT-GGTTGACCCAGTACACCATCC 1394  
 DB 660 CACTGTGACCAACAGGCTTCTCTCTCCGAGACATGAGGTGACAGTACACCATCC 719  
 OY 1395 TCAGCTTAAGTTAGAGGCTTAATTCGAC--TCCTACATATATATGATTTGTCTTACCA 1452  
 DB 720 TCAGCTTAAGTTAGAGGCTTAATTCGACGCGCTTACCAAGATATCATTTGTCTTACCA 779  
 OY 1453 AACAC-CCCTTAGCTC-CCCTTAGCTACATATGATCTACTGCTCCCTGACC 1506  
 DB 780 AACACCCCTTAGCTCTCCCTTAGCTACATATGATCTA-TCTGGCTCCCTGACC 834

RESULT 5  
 B1328115 758 bp mRNA linear EST 30-JUL-2001  
 LOCUS 602979264F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:5132391 5',  
 DEFINITION mRNA sequence.  
 ACCESSION B1328115  
 VERSION B1328115.1 GI:15012772  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 758)  
 AUTHORS NIH-MGC <http://mgc.ncl.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: Jeffrey E. Green, M.D.  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Plate: L1M11324 row: c column: 16  
 High quality sequence stop: 758.  
 Location/Qualifiers

FEATURES  
 Source 1..758  
 /organism="Mus musculus"  
 /strain="FVB/N"  
 /db\_xref="taxon:10090"  
 /clone="IMAGE:5132391"  
 /clone\_lib="NCI CGAP\_L19"  
 /lab\_host="DH10B (TI phage-resistant)"  
 /note="Organ: Liver; Vector: pCMV-Sport6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP Library."

BASE COUNT 168 a 229 c 194 g 167 t

Query Match 45.4%; Score 706.6; DB 10; Length 758;  
 Best Local Similarity 98.4%; Pred. No. 3e-186;  
 Matches 745; Conservative 0; Mismatches 9; Indels 3; Gaps 3;

OY 40 AGGTCCTCTGTCGCGCCAGACAGAGTTGAAG-CACTCCTCTGTAGACCCTGAATATAGGC 98  
 DB 1 AGGTCCTCTGTCGCGCCAGACAGAGTTGAAGCCATCTCCCTGTAGACCCTGAATATAGGC 60  
 OY 99 TTTGGGCTCTTAAGAGGCTATCCCTCCAGCAATGCGCTCTCTGCTCTGCTCTTC 158  
 DB 61 TTTGGGCTCTTAAGAGGCTATCCCTCCAGCAATGCGCTCTCTGCTCTGCTCTTC 120

Y	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	524	525	526	527	528	529	530	531	532	533	534	535	536	537	538	539	540	541	542	543	544	545	546	547	548	549	550	551	552	553	554	555	556	557	558	559	560	561	562	563	564	565	566	567	568	569	570	571	572	573	574	575	576	577	578	579	580	581	582	583	584	585	586	587	588	589	590	591	592	593	594	595	596	597	598	599	600	601	602	603	604	605	606	607	608	609	610	611	612	613	614	615	616	617	618	619	620	621	622	623	624	625	626	627	628	629	630	631	632	633	634	635	636	637	638	639	640	641	642	643	644	645	646	647	648	649	650	651	652	653	654	655	656	657	658	659	660	661	662	663	664	665	666	667	668</
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Query Match	Best Local Similarity	Matches	786:	Conservative	0:	Mismatches	20:	Indels	8:	Gaps	7:
1. 823	44.7%	Score 696:	DB 10:	length 833:							
/organism="Mus musculus"	/strain="FVB/N"	/db_xref="taxon:10090"	/clone="IMAGE:4212125"	/clone_lib="NCI CGAP L19"	/lab_host="DH10B (TI phage-resistant)"	/note="organ: liver; Vector: pcMV-Spork6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI CGAP library."					
BASE COUNT	181 a	247 c	221 g	174 t							
ORIGIN											
Query Match	Best Local Similarity	Matches	786:	Conservative	0:	Mismatches	20:	Indels	8:	Gaps	7:
46	CCTGTGCCCCAGAGACAGAGTTGAAG-CACCTCCCGTTGAGACCCCTGAATATAGCCTTTGGG	104	4	CCGTGTGCCAGACAGAGTTGAAGCCACTCCCGTTGAGACCCCTGAATATAGAGC-TTGGG	62	105	TCCCTTAAAGAGGCTATCCCTCAGCAATGGCCTCCTCTTGGCTCTGCTGCTCTTCTGTTCC	164	63	TCCCTTAAAGAGGCTATCCCTCAGCAATGGCCTCCTCTTGGCTCTGCTGCTCTTCTGTTCC	122
165	TGACCTCCACACAGAGTGTGAACCCCAAACTGAGGGTCCATGCCACAGATGTTGGGGTG	224	123	TGACCTCCACACAGAGTGTGAACCCCAAACTGAGGGTCCATGCCACAGATGTTGGGGTG	182	225	CCATCTTTGACCTGGAGAGCCAGCGGAGCTCTTCGATTTGGCCAAATAAAGTATCC	284	183	CCATCTTTGACCTGGAGAGCCAGCGGAGCTCTTCGATTTGGCCAAATAAAGTATCC	241
285	TGAGACAAGCTGCACCTAGAGCCAGCGCCCATACTAGTGGCCAGTGTCCAGAGGGGCTC	344	242	TGAGACAAGCTGCACCTAGAGCCAGCGCCCATACTAGTGGCCAGTGTCCAGAGGGGCTC	301	345	TCAAGACCGGCGTGCAGCGCCTCCGGGGGCTTCGACGGGAAACCTGTTGGAGCATGACC	404	302	TCAAGACCGGCGTGCAGCGCCTCCGGGGGCTTCGACGGGAAACCTGTTGGAGCATGACC	361
405	AGAGACAGAAAGATATGATGATCATCAGCTTTGCTGACACAGACTCTCCAGCATCAACC	464	362	AGAGACAGAAAGATATGATGATCATCAGCTTTGCTGACACAGACTCTCCAGCATCAACC	421	465	AGACCCGGGCTCGAATTCATCTCTGTGTGAATGGCCAGTGGCATGGATGCCGGAGA	524	422	AGACCCGGGCTCGAATTCATCTCTGTGTGAATGGCCAGTGGCATGGATGCCGGAGA	481
525	CCGGCTTCATGTTTGTGTGAGTTCCGCCACAATGCCACCCAGACATGAATTAAGAG	584	482	CCGGCTTCATGTTTGTGTGAGTTCCGCCACAATGCCACCCAGACATGAATTAAGAG	541	585	TTCTTTGCTAAGACATATGACACCAA--CCCTGACCTTTGACAAAGTCAAGTCACTGTGCA	642	542	TTCTTTGCTAAGACATATGACACCAA--CCCTGACCTTTGACAAAGTCAAGTCACTGTGCA	601
602	GGTGAATGCGAGTGGCTGTACACCACTTCTCCGGAGCCGTAAGCTCAACCTG-TTGCAG	660	703	CCAGGACACCTTACTCTGAGAGCTGTACAGAAAGCAGAGTGGCCACAGTCTCTTGAT	762	703	CCAGGACACCTTACTCTGAGAGCTGTACAGAAAGCAGAGTGGCCACAGTCTCTTGAT	720	763	CCAGGACACCTTACTCTGAGAGCTGTACAGAAAGCAGAGTGGCCACAGTCTCTTGAT	720
721	CCGTGGGCTGTGTTCCACAGAGCCCTTTGTTGGAGGCCA-GTAAGGGTTGAGGCCA-CC	778	823	TGCGGTTGCGCGGAGAGTATGATGCGAGGG	856	823	TGCGGTTGCGCGGAGAGTATGATGCGAGGG	856	779	TCCGGTTGCGCGGAGAGTATGATGCGAGGGG	812

RESULT 7  
BF232704 816 bp mRNA linear EST 14-NOV-2000  
LOCUS 602023292F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4158766 5',  
DEFINITION mRNA sequence.  
ACCESSION BF232704  
VERSION BF232704.1 GI:11142342  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: c9pbbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L19M9435 row: 9 column: 23  
High quality sequence stop: 714.  
Location/Qualifiers  
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/strain="FVB/N"  
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/lab\_host="NCI\_CGAP\_L19"  
/note="Organ: Liver; Vector: pCMV-SPORT6; Site: 1; NotI;  
Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 167 a 253 c 221 g 175 t  
ORIGIN  
Query Match 42.0%; Score 653.8; DB 10; Length 816;  
Best Local Similarity 97.5%; Pred. No. 1.8e-171;  
Matches 738; Conservative 0; Mismatches 12; Indels 7; Gaps 7;  
OY 26 GTCACTTCCTCCAGAGGCTCCTGTGACGAGACAGAGTTGAAG-CATCCCGTTGAGA 84  
DB 1 GTCACTTCCTCCAGAGGCTCCTGTGACGAGACAGAGTTGAAGCAAGCCATCCCGTTGAGA 59  
OY 85 CCCGTAATATAGGCTTTGGGCTTTAAGAGGCTATCTCCAGCAATGCGCTCTCTT 144  
DB 60 CCCGTAATATAGGCTTTGGGCTTTAAGAGGCTATCTCCAGCAATGCGCTCTCTT 118  
OY 145 GCTCTGCTCTTCTGTTCTGCTGCTCAACACAGTAGTAACCCCAAACTGAGGCTC 204  
DB 119 GCTCTGCTCTTCTGTTCTGCTGCTCAACACAGTAGTAACCCCAAACTGAGGCTC 178  
OY 205 ATGCCACAGATGTTGGGTCATCTTTGACCTGGAGAGCCAGCGGAGGCTGCTTCTGA 264  
DB 179 ATGCCACAGATGTTGGGTCATCTTTGACCTGGAGAGCCAGCGGAGGCTGCTTCTGA 238  
OY 265 TTGGGCCAAGAAATATCTGACCAAGCTGCACTCAGCCAGCCGCCCATATCTAGTGC 324  
DB 239 TTGGGCCAAGAAATATCTGACCAAGCTGCACTCAGCCAGCCGCCCATATCTAGTGC 298  
OY 325 GCCAGTGTCCAGAGGGGCTCTCAAGACCGGCTGACAGCGGCTCCGGGGCTCGACGCA 384  
DB 299 GCCAGTGTCCAGAGGGGCTCTCAAGACCGGCTGACAGCGGCTCCGGGGCTCGACGCA 358  
OY 385 AACCTGTGGAGCATGACGACAGACAGAAATATGAGATCATCAGCTTTGCTGACAC 444

DB 359 AACCTGTGGAGCATGACGACAGACAGAAATATGAGATCATCAGCTTTGCTGACAC 418  
OY 445 AGACCTCTCCAGCATCAACACAGCCGGCTCGAGTTCCCACTTCTGTGTGAATGGCCAG 504  
DB 419 AGACCTCTCCAGCATCAACACAGCCGGCTCGAGTTCCCACTTCTGTGTGAATGGCCAG 478  
OY 505 TGGCATGAGAGTCCGGCAGAGCCGCTTCATGTTCTTCTGTCAGCTTCCCAATGCGAC 564  
DB 479 TGGCATGAGAGTCCGGCAGAGCCGCTTCATGTTCTTCTGTCAGCTTCCCAATGCGAC 538  
OY 565 CCAGACCATGAAATATGAAGTTCTGTGTAAGACCATATGACACCACTCAGCTTTCAC 624  
DB 539 CCAGACCATGAAATATGAAGTTCTGTGTAAGACCATATGACACCACTCAGCTTTCAC 598  
OY 625 AAGTCAGTACGAGTGGTGAATGCAAGTGGCTGTAACCACTTCTCTGGAGCTTGA 684  
DB 599 CAGTCAGTACGAGTGGTGAATGCAAGTGGCTGTAACCACTTCTCTGGAGCTTGA 658  
OY 685 AGC-TCAAGCTGCTTGA-CGCCAGGACACCTTAC-TCTGAGCTGTGACAGAAAGCA 741  
DB 659 AGCTTCAAGCTGCTTGA-CGCCAGGACACCTTAC-TCTGAGCTGTGACAGAAAGCA 717  
OY 742 GGTGGCCCAAGTTCCTTGATCTGAGCTGGCTGTTTCC 778  
DB 718 GGTGGCCCAAGTTCCTTGATCTGAGCTGGCTGTTTCC 754  
RESULT 8  
BF533968 975 bp mRNA linear EST 11-DEC-2000  
LOCUS 602075129F1 NCI\_CGAP\_L19 Mus musculus cDNA clone IMAGE:4212175 5',  
DEFINITION mRNA sequence.  
ACCESSION BF533968  
VERSION BF533968.1 GI:11621331  
KEYWORDS EST.  
SOURCE house mouse.  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: c9pbbs-remail.nih.gov  
Tissue Procurement: Jeffrey E. Green, M.D.  
cDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L19M9782 row: 1 column: 08  
High quality sequence stop: 659.  
Location/Qualifiers  
1. 975  
/organism="Mus musculus"  
/strain="FVB/N"  
/db\_xref="taxon:10090"  
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Site: 2; SalI; Cloned unidirectionally. Primer: Oligo dt.  
Average insert size 1.9 kb. Constructed by Life  
Technologies. Note: this is a NCI\_CGAP Library."  
BASE COUNT 190 a 297 c 266 g 222 t  
ORIGIN  
Query Match 41.3%; Score 643.6; DB 10; Length 975;  
Best Local Similarity 97.2%; Pred. No. 1.4e-168;  
Matches 698; Conservative 0; Mismatches 14; Indels 6; Gaps 4;





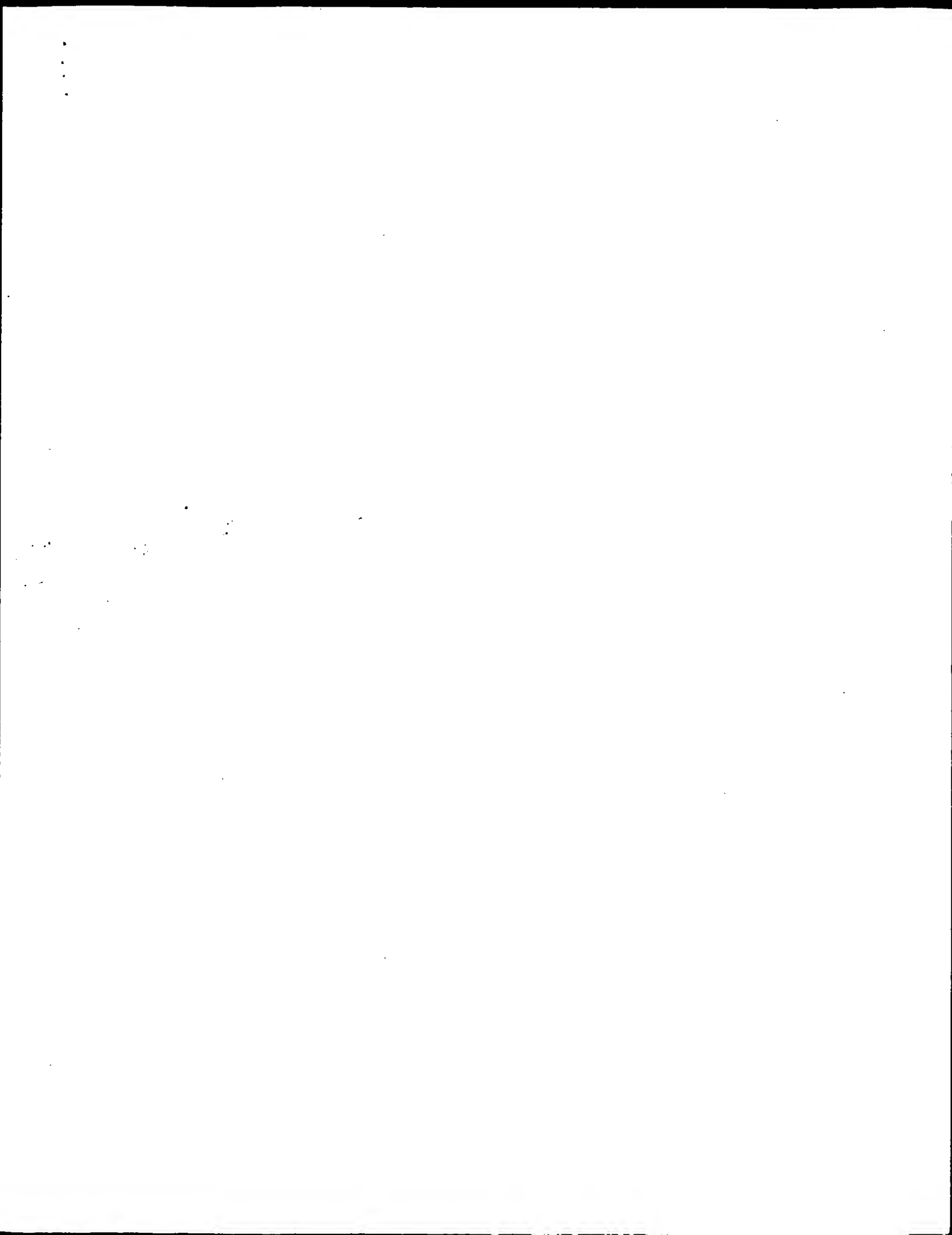












GenCore version 5.1.3  
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# OM protein - protein search, using sw model

Run on: October 11, 2002, 22:15:33 : Search time 41 Seconds  
(without alignments)  
933.609 Million cell updates/sec

Title: US-09-684-383-4

Perfect score: 1850  
Sequence: 1 MASSLLALLFLPTTVVNP.....DSNIVKTDIPDMVEACGCS 352

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.\*  
2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1844	99.7	352	19	AAW60617 Murine liver activ
2	1398	75.6	352	17	AAAR9729 Transforming growt
3	1387	75.0	352	12	AAAR70530 Human TGF-beta M1
4	594	32.1	350	17	AAAR92754 Human growth diffe
5	594	32.1	350	22	AAAR93672 Human polypeptide,
6	585	31.6	350	19	AAAW60619 Human liver activi
7	581.5	31.4	350	19	AAAW60618 Murine liver activi
8	550.5	29.8	427	8	AAAP70200 Sequence of porcine
9	548.5	29.6	407	21	AAAY92017 Human inhibin B su
10	548.5	29.6	407	21	AAAY92017 Human inhibin B su
11	543	23.4	353	8	AAAP70204 Sequence of human

12	540	29.2	426	8	AAAP70203	Sequence of human
13	540	29.2	426	21	AAAY92016	Human inhibin A be
14	540	29.2	426	21	AAAY92018	Human activin A su
15	538	29.1	426	11	AAAR05413	BUF-3 human differ
16	531	28.7	351	8	AAAP70201	Sequence of porcine
17	450	24.3	127	12	AAAR10991	Xenopus Bone Morph
18	444	24.0	87	14	AAAR45447	TGF-beta-like clon
19	440.5	23.8	303	22	AAAU02908	Angiotensin conver
20	431	23.3	288	7	AAAP60518	Sequence of bovine
21	401.5	21.7	121	22	AAAB73203	Inhibin beta C-C
22	398	21.5	122	22	AAAB73202	Inhibin beta C-C
23	396	21.4	130	7	AAAP60520	Sequence of human
24	374.5	20.2	115	13	AAAR26482	Activin-like pepit
25	374	20.2	116	13	AAAR26481	Activin-like pepit
26	373.5	20.2	115	13	AAAR25129	Human KHM-5M, hom
27	373.5	20.2	115	14	AAAR31623	BUF-4, Synthetic,
28	373.5	20.2	116	13	AAAR25127	Activin B, Synthe
29	372	20.1	130	12	AAAR10990	Xenopus Bone Morph
30	371	20.1	116	8	AAAP71196	Sequence of verteb
31	371	20.1	116	8	AAAP71176	Second protein cha
32	371	20.1	116	9	AAAP80019	Sequence of the 14
33	371	20.1	116	9	AAAP82061	Polypeptide BUF-3
34	371	20.1	116	11	AAAR05443	Monomer A of BUF-4
35	371	20.1	116	11	AAAR08215	Follicle stimulat
36	371	20.1	116	13	AAAR25128	Activin AB, Synth
37	371	20.1	116	14	AAAR31622	BUF-3, Synthetic,
38	371	20.1	116	21	AAAP67949	Human activin A SE
39	368.5	19.9	115	8	AAAP71197	Sequence of verteb
40	368.5	19.9	115	8	AAAP71177	Second protein cha
41	368.5	19.9	115	11	AAAR08216	Follicle stimulat
42	368	19.9	116	12	AAAR12088	16.5 kd subunit of
43	363.5	19.6	115	9	AAAP80020	Sequence of the 14
44	363	19.6	116	11	AAAR05444	Monomer B of BUF-4
45	359	19.4	116	9	AAAP81906	N-terminal of inh1

## ALIGNMENTS

RESULT 1	AAW60617	standard; Protein: 352 AA.
ID	AAW60617	
XX	AAW60617	
AC	AAW60617	
XX	01-FEB-1999	(first entry)
DT	01-FEB-1999	
XX		
DE	Murine liver activin beta c polypeptide.	
XX		
KW	Liver activin; beta c; beta e; cell differentiation; hematopoiesis;	
KW	erythroid; ovarian follicular maturation; hormone; neuronal survival;	
KW	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;	
KW	osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosup;	
XX	menstrual disorder; transgenic; modulator.	
XX		
OS	Mus sp.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Peptide	1..20
FT	Modified-site	/note="signal sequence"
FT	Modified-site	111..113
FT	Modified-site	/note="Asn is putatively N-glycosylated"
FT	Modified-site	143..145
FT	Modified-site	/note="Asn is putatively N-glycosylated"
FT	Modified-site	161..163
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FT	Domain	21..236
FT	Domain	/note="propeptide domain"
FT	Cleavage-site	230..236
FT	Cleavage-site	/note="endoproteolytic cleavage site"
FT	Domain	237..352

FT XX /note- "mature growth factor domain"  
 PN XX WO9822492-A1.  
 PD XX 28-MAY-1998.  
 XX XX  
 XX PF 20-NOV-1997; 97WO-US20882.  
 XX XX  
 XX PR 20-NOV-1996; 96US-0752919.  
 XX XX  
 XX PA (UNMI) UNTV MICHIGAN.  
 XX XX  
 PI Bonadio J, Fang J;  
 XX  
 DR WPI: 1998-312408/27.  
 DR N-PSDB: AAV38237.  
 XX  
 PT New isolated nucleic acid encoding sub-units of liver activin -  
 PT useful for regulating growth and differentiation of cells, e.g. for  
 PT treating liver, bone and hematopoietic disorders  
 XX  
 XX PS Claim 16; Fig 1: 141pp; English.  
 XX  
 CC This represents a murine liver activin beta c polypeptide. Sequences  
 CC derived from beta c cDNA clone is used for screening and cloning a liver  
 CC activin beta c gene. Disorders of cell growth or differentiation (or  
 CC susceptibility to them) are diagnosed by measuring liver activin gene  
 CC activity or by detecting a mutation in the liver activin gene. Disorders  
 CC of hematopoiesis, erythroid differentiation, ovarian follicular  
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone  
 CC formation, insulin secretion or cardiac morphogenesis are some conditions  
 CC that can be diagnosed using the liver activin. Cell growth and  
 CC differentiation can be stimulated by treatment with an liver activin  
 CC compound or agent that upregulates the compound's expression. Antagonists  
 CC can be used to treat liver diseases while agonists can be used to  
 CC increase growth and regeneration of liver tissue. The liver activin  
 CC compound may also induce bone growth (e.g. for treating osteoporosis or  
 CC osteomalacia) or hematopoiesis, particularly erythropoiesis, e.g. for  
 CC treating hemophilia, cystic fibrosis or menstrual disorders. Antibodies  
 CC are useful in immunoassays, to generate anti-idiotypic antibodies (which  
 CC bind to liver activin receptors) and to inhibit liver activin. Also,  
 CC transgenic animals containing liver activin gene can be used to produce  
 CC the liver activin (in correctly processed and modified forms) proteins,  
 CC or the transgenic animals, are useful for screening for liver activin  
 CC modulators.  
 CC  
 XX Sequence 352 AA:  
 XX  
 Query Match 99.7%; Score 1844; DB 19; Length 352;  
 Best Local Similarity 99.7%; Pred. No. 2.9e-169;  
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

DB 301 LKANAAGTTGRGCCVPTSRRLSLIYDROSDNIVKTDIPDMVVEACGCS 352  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 RESULT 2  
 ID AAR89729  
 XX AAR89729 standard; Protein; 352 AA.  
 XX  
 XX AC AAR89729;  
 XX  
 DT 09-AUG-1996 (first entry)  
 XX  
 DE Transforming growth factor beta MP-121.  
 XX  
 XX KW TGF-beta; MP-121; mitogen; differentiation; induction; promotion;  
 KW maintenance; morphogen; tissue regeneration; dental implantation;  
 KW wound healing.  
 XX  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FH Protein 237..352  
 FT /label= mature-protein  
 XX  
 XX DEJ9511243-A1.  
 XX  
 XX PN 04-JAN-1996.  
 XX  
 XX PD 27-MAR-1995; 95DE-1011243.  
 XX  
 XX PF 01-JUL-1994; 94DE-1423190.  
 XX  
 XX PR (BIOP-) BIOPHARM GES BIOTECHNOLOGISCHEN ENTWICKL.  
 XX  
 XX PI Bechtold R, Neidhardt H, Pohl J, Hoelten G;  
 XX  
 XX DR WPI: 1996-050788/06.  
 DR N-PSDB: AAT11104.  
 XX  
 PT DNA encoding transforming growth factor beta MP-121 - has mitogenic  
 PT and differentiation-inducing activity, e.g. for use in wound healing  
 XX  
 XX PS Claim 7; Page 11; 15pp; German.  
 XX  
 CC A cDNA library prepared using total RNA from human liver was  
 CC subjected to PCR amplification using primers corresp. to conserved  
 CC regions within the TGF-beta family. Amplification products were  
 CC subcloned and sequenced; one clone (designated psk-MP121) was found  
 CC to contain a new sequence. Part of the insert from the clone was  
 CC used to re-screen the human liver cDNA library and a 2272 bp fragment  
 CC coding for a TGF-beta-like protein (i.e. the present sequence) was  
 CC isolated. This protein has mitogenic and differentiation-inducing  
 CC properties making it (or fusion proteins comprising it or heterodimers  
 CC of the protein with a cystine knot motif protein) useful for inducing  
 CC tissue regeneration, e.g. for wound healing, inducing growth of  
 CC hepatic tissue or bone marrow precursor cells, treating fertility  
 CC disorders, etc.  
 CC  
 XX Sequence 352 AA:  
 XX  
 Query Match 75.6%; Score 1398; DB 17; Length 352;  
 Best Local Similarity 76.2%; Pred. No. 2.7e-126;  
 Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

Db 120 SDRTAGREVOASLMFEVQPSNTWTWTLKRVVLGPHNTLTLATQYLLEVDASGMHQ 179  
 Qy 180 LLLGPEAOACSGHLLTELVEPESOVANSSLLGMSHRRPFAAARVRECKHRRRGID 239  
 Db 180 LPLGPEAOACSGHLLTELVEPESOVANSSVILGGAHRPFVAARVRECKHRRRGID 239  
 Qy 240 CCGSRMCCROEFVDFRIGNDWITIOPEGYAMNFCIGCPHIVAGMPGISAFHTAVL 299  
 Db 240 CCGSRMCCROEFVDFRIGNDWITIOPEGYAMNFCIGCPHIVAGMPGISAFHTAVL 299  
 Qy 300 NLKANAAGTGTGRGSCCVPTRRPLSLLYDRDSNIVKTDIDPMVVEACGS 352  
 Db 300 NLKANAAGTGTGRGSCCVPTRRPLSLLYDRDSNIVKTDIDPMVVEACGS 352  
 RESULT 3  
 AAB70530  
 ID AAB70530 standard; Protein: 352 AA.  
 AC AAB70530:  
 DT 08-MAY-2001 (first entry)  
 DE Human TGF-beta MP121 protein sequence SEQ ID NO:4.  
 XX  
 XX Human: transforming growth factor-beta; monomeric protein; MP52;  
 KM MP121; dimeric protein; TGF-beta; osteoporosis; osteoporosis; bone;  
 KW neuroprotection; anti-inflammation; gene therapy; bone;  
 KW cartilage; dental; wound healing; connective tissue.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Misc-difference 316  
 FT /note="unspecified"  
 XX  
 PN EPI074620-A1.  
 XX  
 PD 07-FEB-2001.  
 XX  
 PF 06-AUG-1999; 99EP-0115613.  
 XX  
 PF 06-AUG-1999; 99EP-0115613.  
 XX  
 PR (HUGE-) HYGENE AG C/O MAEDER & BAUMGARTNER TREUH.  
 XX  
 PA MPI: 2001-228100/24.  
 DR N-PSDB: AAF74421.  
 DR  
 DR Novel monomeric protein of transforming growth factor-beta family for  
 PT prevention or therapy of diseases associated with bone, cartilage  
 PT damage, promotion of wound healing, has substitution or deletion of  
 PT cysteine -  
 XX  
 PS Claim 10; Page 21-22; 31pp; English.  
 XX  
 XX The present invention describes a protein (I) selected from the members  
 CC of the transforming growth factor-beta (TGF-beta) superfamily, which is  
 CC monomeric due to substitution or deletion of a cysteine which is  
 CC responsible for dimer formation. Also described are: (1) nucleic acid  
 CC (II) encoding (I); (2) expression vector (III) containing (II) in a  
 CC suitable vector system; (3) host cell (IV) containing (III) capable of  
 CC producing (I); and (4) a pharmaceutical composition (V) containing (I);  
 CC (II), (III) or (IV). (I) has a pharmacological activity, neurotrophic,  
 CC neuroprotective, anti-inflammation and osteoporosis activities, and can be  
 CC used in gene therapy. (V) is useful for the prevention or therapy of  
 CC diseases for which also the dimeric form of the protein would be  
 CC indicated. Diseases treatable include diseases associated with bone  
 CC and/or cartilage damage or affecting bone and/or cartilage disease or  
 CC situations in which cartilage and/or bone growth is desirable, for spinal  
 CC fusion, for damaged or diseased tissue associated with connective tissue  
 CC including tendon and/or ligament, periodontal or dental tissue including

CC dental implants, neural tissue including CNS tissue and neuropathological  
 CC situations, tissue of the sensory system, liver, pancreas, cardiac,  
 CC blood vessel, renal, uterine and thyroid tissue, skin, mucous membrane,  
 CC endothelium, epithelium, for promotion or induction of nerve growth,  
 CC tissue regeneration, angiogenesis, wound healing including ulcers, burns,  
 CC injuries or skin grafts, induction of proliferation of progenitor cells  
 CC or bone marrow cells, for maintenance of a state of proliferation or  
 CC differentiation, for treatment or preservation of tissue or cells for  
 CC organ or tissue transplantation, for integrity of gastrointestinal lining  
 CC and for treatment of disturbances in fertility, contraception or  
 CC pregnancy. The present sequence represents the specifically claimed  
 CC TGF-beta monomeric protein MP121, from the present invention.  
 XX  
 SQ Sequence 352 AA;  
 XX  
 Query Match 75.0%; Score 1387; DB 22; Length 352;  
 Best Local Similarity 75.9%; Pred. No. 3,1e-125;  
 Matches 268; Conservative 32; Mismatches 51; Indels 2; Gaps 2;  
 Qy 1 MASSLLALLFLPTTVVNPKEGCPACWGAIFDLBESORELLDLAKKSIDKHLRSR 60  
 Db 1 MTSSLLAFLLAPTVVATPRACGCPGLELESORELLDLAKKSIDKHLRSR 60  
 Qy 61 PILSRPVSRGALKTAOLRGRPRETLEHDOREBEYELISFADPDLSSINOTRLEPHRS 120  
 Db 61 PTLNRPVSRRAALRLALOHIGHVPGALLE-DNREDECEIISFRETGLSTINOTRLEPHRS 119  
 Qy 121 G-RMASGMEVROTREPMPVOPFPNATQFMNIVLVLPYDTNLTSTQVVOVNASGMWY 179  
 Db 120 SDRTAGREVOASLMFEVQPSNTWTWTLKRVVLGPHNTLTLATQYLLEVDASGMHQ 179  
 Qy 180 LLLGPEAOACSGHLLTELVEPESOVANSSLLGMSHRRPFAAARVRECKHRRRGID 239  
 Db 180 LPLGPEAOACSGHLLTELVEPESOVANSSVILGGAHRPFVAARVRECKHRRRGID 239  
 Qy 240 CCGSRMCCROEFVDFRIGNDWITIOPEGYAMNFCIGCPHIVAGMPGISAFHTAVL 299  
 Db 240 CCGSRMCCROEFVDFRIGNDWITIOPEGYAMNFCIGCPHIVAGMPGISAFHTAVL 299  
 Qy 300 NLKANAAGTGTGRGSCCVPTRRPLSLLYDRDSNIVKTDIDPMVVEACGS 352  
 Db 300 NLKANAAGTGTGRGSCCVPTRRPLSLLYDRDSNIVKTDIDPMVVEACGS 352  
 RESULT 4  
 AAR92754  
 ID AAR92754 standard; Protein: 350 AA.  
 AC AAR92754:  
 DT 21-JUL-1996 (first entry)  
 DE Human growth differentiation factor-12.  
 XX  
 DE Human growth differentiation factor-12.  
 XX  
 KW Growth differentiation factor-12; GDF-12; liver; cell proliferation;  
 KW cancer; diagnosis; therapy; transforming growth factor beta.  
 XX  
 OS Homo sapiens.  
 FH Key Location/Qualifiers  
 FT Modified-site 198..200  
 FT /label= N-glycosylation\_site  
 FT Cleavage-site 232..236  
 FT Region 237..350  
 FT /label= C-terminal\_region  
 FT /note= "GFR-12 active C-terminal fragment"  
 XX  
 PN MO9602559-A1.  
 XX  
 PD 01-FEB-1996.  
 XX  
 PF 12-JUL-1995; 95WO-US08745.  
 XX



PR 26-SEP-1994; 94US-0311370.  
 PR 13-JUL-1994; 94US-0274215.  
 XX  
 PA (UYJO ) UNIV JOHNS HOPKINS SCHOOL MED.  
 XX  
 PI Esqueja AF, Lee S;  
 XX  
 DR WPI: 1996-105850/11.  
 DR N-PSDB: AAT16883.  
 XX  
 PT DNA encoding Growth Differentiation Factor-12 - used in diagnostic  
 PT and therapeutic methods esp. in methods for treating a cell  
 PT proliferative disorder of liver origin  
 XX  
 PS Claim 3; Page 40-43; 52pp; English.  
 XX  
 CC Human growth differentiation factor-12 (GDF-12 - AAR92754) is a new  
 CC member of the transforming growth factor beta superfamily that is  
 CC expressed specifically in liver. It can be obt. by expression  
 CC of a cDNA clone (AAT16883) derived from adult liver in transformed  
 CC host cells. GDF-12 possesses activities that will make it useful  
 CC in the treatment of liver disorders, e.g. disease states in which  
 CC liver function is compromised, or cellular proliferative disorders  
 CC such as hepatocellular carcinoma. In can also be used to expand  
 CC liver cells in culture and to raise diagnostic antibodies.  
 CC  
 XX  
 SO Sequence 350 AA:  
 Query Match 32.1%; Score 594; DB 17; Length 350;  
 Best Local Similarity 39.3%; Pred. No. 8.2e-49;  
 Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;  
 OY 22 TEGPCACGAIPTDESORELIDLAKKSLIDKLHLSORPLSRVSGALKTALQRLR- 80  
 DB 22 TGSVCPCGSGSKLAPQAEALVLELAKQOILDLHLSRRIRHPPOALTRALRLRQP 81  
 OY 81 ---GPRRETLLEHDOOEYEITSEAD-TDLSSINOTRLEHFGSRMASGMEVROTFRMF 136  
 DB 82 GSAVAPNGE-----EVLISFATVTDSTSAVSSLTFTFLS--TPRSHHLYHARLWL 128  
 OY 137 FVQFPNNATOTMNI-----RVLYLRPYDNLTLTSTQYVYVNASGWYQLLGP 184  
 DB 129 HVLPTLPGLCLRIFRMGPRRRRQSGRTLLAEHHTNL-----GMHTTLTLP 175  
 OY 185 EAQACSGOGLTLELVESOVANSSL-----ILGFSSH-RPFAAQRVRE--GKHRYR 235  
 DB 176 SGLRGEKSGVLKIQDLCRLDCEGNSVTGQPRRLDTAGHOQPLLEKIRANEGAGRARR 235  
 OY 236 RGIDCGGSRMCCROEFVDFREIGNNDWIIOPEGYAMNCTGQCPPLHVAAGMGISASFH 295  
 DB 236 RPTTCEPATPLCCRRDHYVDFQELGMDWILQPEGYOLNVCSGCCPHLAGSGIAASFH 295  
 OY 296 TAVNLILKANA--AAGTTGRCSCVPTSRRLSLIYYDSDSNIVKTDIDPMVVEACGCS 352  
 DB 296 SAVFSLKANNPWPAST-----SCCVPTARRPLSLIYLDHNGVNVKTDVPMVVEACGCS 350  
 RESULT 5  
 AAM93672  
 ID AAM93672 standard; Protein: 350 AA.  
 XX  
 AC AAM93672;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human polypeptide, SEQ ID NO: 3558.  
 XX  
 KM Human: full length cDNA; cDNA synthesis: oligo-capping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1130094-A2.  
 XX

PD 05-SEP-2001.  
 XX  
 PF 07-JUL-2000; 2000EP-0114089.  
 XX  
 PR 08-JUL-1999; 99JP-0194486.  
 PR 11-JAN-2000; 2000JP-0118774.  
 PR 02-MAY-2000; 2000JP-0183765.  
 XX  
 PA (HELI-) HELIX RES INST.  
 XX  
 PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;  
 PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;  
 XX  
 DR WPI: 2001-524255/58.  
 DR N-PSDB: AAK94607.  
 XX  
 PT 830 Primers useful for synthesizing full length cDNA clones and their  
 PT use in genetic manipulation -  
 XX  
 PS Claim 8; SEQ ID NO 3558; 1380pp + sequence listing; English.  
 XX  
 CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been  
 CC isolated and nucleotide sequences of 5' - and 3' - ends of the cDNA  
 CC molecules have been determined. Primers for synthesizing the full length  
 CC cDNA are useful for clarifying the function of the protein encoded by  
 CC the cDNA. The full length clones were obtained by construction of full  
 CC length enriched cDNA libraries that were synthesised by the oligo-capping  
 CC method. The primers enable the production of the full length cDNA easily  
 CC without any special methods. The present sequence is a polypeptide  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in CD-ROM format directly from EPO.  
 CC  
 XX  
 SO Sequence 350 AA:  
 Query Match 32.1%; Score 594; DB 22; Length 350;  
 Best Local Similarity 39.3%; Pred. No. 8.2e-49;  
 Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;  
 OY 22 TEGPCACGAIPTDESORELIDLAKKSLIDKLHLSORPLSRVSGALKTALQRLR- 80  
 DB 22 TGSVCPCGSGSKLAPQAEALVLELAKQOILDLHLSRRIRHPPOALTRALRLRQP 81  
 OY 81 ---GPRRETLLEHDOOEYEITSEAD-TDLSSINOTRLEHFGSRMASGMEVROTFRMF 136  
 DB 82 GSAVAPNGE-----EVLISFATVTDSTSAVSSLTFTFLS--TPRSHHLYHARLWL 128  
 OY 137 FVQFPNNATOTMNI-----RVLYLRPYDNLTLTSTQYVYVNASGWYQLLGP 184  
 DB 129 HVLPTLPGLCLRIFRMGPRRRRQSGRTLLAEHHTNL-----GMHTTLTLP 175  
 OY 185 EAQACSGOGLTLELVESOVANSSL-----ILGFSSH-RPFAAQRVRE--GKHRYR 235  
 DB 176 SGLRGEKSGVLKIQDLCRLDCEGNSVTGQPRRLDTAGHOQPLLEKIRANEGAGRARR 235  
 OY 236 RGIDCGGSRMCCROEFVDFREIGNNDWIIOPEGYAMNCTGQCPPLHVAAGMGISASFH 295  
 DB 236 RPTTCEPATPLCCRRDHYVDFQELGMDWILQPEGYOLNVCSGCCPHLAGSGIAASFH 295  
 OY 296 TAVNLILKANA--AAGTTGRCSCVPTSRRLSLIYYDSDSNIVKTDIDPMVVEACGCS 352  
 DB 296 SAVFSLKANNPWPAST-----SCCVPTARRPLSLIYLDHNGVNVKTDVPMVVEACGCS 350  
 RESULT 6  
 AAM60619  
 ID AAM60619 standard; Protein: 350 AA.  
 XX  
 AC AAM60619;  
 XX  
 DT 01-FEB-1999 (first entry)  
 XX

Accession	Key	Location/Qualifiers	Score	DB	Length	Gaps
XX	Human liver activin beta e polypeptide.		31.6%	585	19	350
XX	Liver activin: beta c; beta e; cell differentiation; haematopoiesis; erythroid; ovarian follicular maturation; hormone; neuronal survival; spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis; osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosassay; menstrual disorder; transgenic; modulator; human.		38.7%	53	109	58
XX	Homo sapiens.					
OS						
XX	Key	1..17				
XX	Peptide	/note="signal sequence"				
XX	Domain	18..236				
XX	Modified-site	/note="propeptide domain"				
XX	FT	198..200				
XX	FT	/note="Asn is putatively N-glycosylated"				
XX	FT	232..236				
XX	Cleavage-site	/note="endoproteolytic cleavage site"				
XX	FT	237..350				
XX	Domain	/note="mature growth factor domain"				
XX	MO9822492-A1.					
XX	28-MAY-1998.					
XX	20-NOV-1997;	97MO-US20882.				
XX	20-NOV-1996;	96US-0752919.				
XX	(UNMT ) UNIV MICHIGAN.					
XX	Bonadio J, Fang J:					
XX	WPI: 1998-312408/27.					
XX	N-PSDB: AAV38240.					
XX	New isolated nucleic acid encoding sub-units of liver activin -					
XX	useful for regulating growth and differentiation of cells, e.g. for					
XX	treating liver, bone and haematopoietic disorders					
XX	Disclosure; Flg 5; 141pp; English.					
XX	This represents a human liver activin beta e polypeptide. The invention					
XX	provides murine beta c and beta e polypeptides and the encoding genes.					
XX	Disorders of cell growth or differentiation (or susceptibility to them)					
XX	are diagnosed by measuring liver activin gene activity or by detecting a					
XX	mutation in the liver activin gene. Disorders of haematopoiesis,					
XX	erythroid differentiation, ovarian follicular maturation, hormone					
XX	secretion, neuronal survival, spermatogenesis, bone formation, insulin					
XX	secretion or cardiac morphogenesis are some conditions that can be					
XX	diagnosed using the liver activin. Cell growth and differentiation can be					
XX	stimulated by treatment with an liver activin compound or agent that					
XX	upregulates the compound's expression. Antagonists can be used to treat					
XX	liver diseases while agonists can be used to increase growth and					
XX	regeneration of liver tissue. The liver activin compound may also induce					
XX	bone growth (e.g. for treating osteoporosis or osteomalacia) or					
XX	haematopoiesis, particularly erythropoiesis, for treating haemophilia,					
XX	cystic fibrosis or menstrual disorders. Antibodies are useful in					
XX	immunosassays, to generate anti-idiotypic antibodies (which bind to liver					
XX	activin receptors) and to inhibit liver activin. Also, transgenic animals					
XX	containing liver activin gene can be used to produce the liver activin					
XX	(in correctly processed and modified forms) proteins, or the transgenic					
XX	animals, are useful for screening for liver activin modulators.					
XX	Sequence 350 AA:					
XX	Query Match	31.6%	Score 585	DB 19	Length 350	
XX	Best Local Similarity	38.7%	Pred. No. 6	1e-48		
XX	Matches 139; Conservative 53; Mismatches 109; Indels 58; Gaps 11					

Accession	Protein Name	Species	Length (aa)	Weight (kDa)	PI	Ref									
Db	22 TGSVPCSGSKLAPQAEALVLELAKQOLLEGILHLSRPRITPPROAAVTRALRLRIP	81													
Oy	81 ---GPRRETLLLEHDQROEYEYIISFAD--TDLSSINQRLERHFSGMASGMEVQTRFMF	136													
Db	82 GSVABNGE-----EVIISFATVDTSTSAVSSLLTFHLS--TPRSHILYHARLML	128													
Oy	137 FVQFPHNATQTMNI-----RVLYLRPYDTNLTLTSQIVVQVNASGHWYOLLGP	184													
Db	129 HVLPLPGLTCLHIFRMGPRRRRQSGRTLLAEHHITNL-----GWHTLTLPS	175													
Oy	185 EDAOACSGGHLTLELYPEISOVAHSSL-----ILGMFSH--RPVNAQVRVE--GKHVRVR	235													
Db	176 SGLRGEKSGVLKQLQDCRPLEGNSVTVGQPRRLDLDTAGHOQPFLELKLIRAMEPGAGRARR	235													
Oy	236 RGLDQGGSGSMCCROEFTVDPERELTGMDWITLOPEGYAMNFTGQCPLHVACMPGISASFH	295													
Db	236 RPTCEPAPPLCCRRDHYVFOELGMDWITLQPEGYQNTYNSGQCPRHLACGPGTIAASFH	295													
Oy	296 TAVNLILKANA--AAGTGTGSGCCVPTSRRLPLSLTYPRDSNIYVTDIPDMVVEACGS	352													
Db	296 SAVESLLKANNPMPAST---SCCVPTARRPLSLLYLDHNGNVYVTDVPDMVVEACGS	350													
Result 7															
AAM60618	AAM60618 standard; Protein: 350 AA.														
XX	AAM60618:														
XX	01-FEB-1999 (first entry)														
XX	Murine liver activin beta e polypeptide.														
DE	Liver activin; beta c; beta e; cell differentiation; haematopoiesis;														
KW	erythroid; ovarian follicular maturation; hormone; neuronal survival;														
KW	spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;														
KW	osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunosuppression;														
KW	menstrual disorder; transgenic; modulator.														
XX															
OS	Mus sp.														
XX															
FH	Key	Location/Qualifiers													
FT	Peptide	1..21													
FT	/note="signal sequence"														
FT	Domain	22..236													
FT	Modified-site	/note="propeptide domain"													
FT	198..200														
FT	/note="Asn is putatively N-glycosylated"														
FT	Cleavage-site	232..236													
FT	/note="endoproteolytic cleavage site"														
FT	Domain	237..349													
FT	/note="mature growth factor domain"														
XX															
PN	W09822492-A1.														
XX															
PD	28-MAY-1998.														
XX															
PF	20-NOV-1997; 97WO-US20882.														
XX															
PR	20-NOV-1996; 96US-0752919.														
XX															
PA	(UNMI ) UNIV MICHIGAN.														
XX															
PI	Bonadio J, Fang J;														
XX															
DR	WPI; 1998-312408/27.														
XX															
DR	N-PSDB; AAV38238.														
XX															

XX This represents a murine liver activin beta e polypeptide. Sequences  
 CC derived from a beta c cDNA clone is used for screening and cloning the  
 CC activin beta e gene. Disorders of cell growth or differentiation (or  
 CC susceptibility to them) are diagnosed by measuring liver activin gene  
 CC activity or by detecting a mutation in the liver activin gene. Disorders  
 CC of haematopoiesis, erythroid differentiation, ovarian follicular  
 CC maturation, hormone secretion, neuronal survival, spermatogenesis, bone  
 CC formation, insulin secretion or cardiac morphogenesis are some conditions  
 CC that can be diagnosed using the liver activin. Cell growth and  
 CC differentiation can be stimulated by treatment with an liver activin  
 CC compound or agent that upregulates the compound's expression. Antagonists  
 CC can be used to treat liver diseases while agonists can be used to  
 CC increase growth and regeneration of liver tissue. The liver activin  
 CC compound may also induce bone growth (e.g. for treating osteoporosis or  
 CC osteomalacia) or haematopoiesis, particularly erythropoiesis, e.g. for  
 CC treating haemophilia, cystic fibrosis or menstrual disorders. Antibodies  
 CC are useful in immunoassays, to generate anti-idiotypic antibodies (which  
 CC bind to liver activin receptors) and to inhibit liver activin. Also,  
 CC transgenic animals containing liver activin gene can be used to produce  
 CC the liver activin (in correctly processed and modified forms) proteins,  
 CC or the transgenic animals, are useful for screening for liver activin  
 CC modulators.

XX Sequence 350 AA:

Query Match 31.4% Score 581.5; DB 19; Length 350;  
 Best Local Similarity 37.7% Pred. No. 1.3e-47;

Matches 140; Conservative 66; Mismatches 110; Indels 55; Gaps 14;

OY 5 LLLALLFTPTTVNPKTEGCPACMGATFDESORELLDLAKKSLDKLHLSRPLLS 64  
 DB 12 LLMALVWV-----QSRASACPSGCGPTLAPGEBRALVLELAQOILEGLHLTSRPT 64  
 OY 65 RPSRQALKTALORLKP-----RETLLEHDQROEYEITSPAD--TDLSSINOTRLE 116  
 DB 65 RPLPQALTRALRLQ--PKSMVPGNRE-----KVISRTIIDKSTSTYRSMLT 111  
 OY 117 FHRSGMASGMEVROTFRMFVOPPHNATOTMIRVLYLRPYDTNL-----TLTSQYVVOV 172  
 DB 112 FOLSLPMSHNL-----YHARLMLHVPSPFPGTLYLR--IFRCGTYRCRGFTFLAEH--QT 163  
 OY 173 NASGMYQLLGPBAQAACSGHLLTEL-----VPESQVHSSLLGLMF--SHRPVAAOV 225  
 DB 164 TSSGMHPLTLPSGLKSEDSGVYKLOLEFRPLDLNSTAACLPLRLDTPAGGQRPFLDKI 223  
 OY 226 RVE--GKRVRRRGIDCGGSRMCROEFVDFREIGMNDWIIOPEGYAMNFCGQCPH 283  
 DB 224 RANEPGAGRARRPTPCETPTLCRRDHYVDFOLCMRWIILQPEGYOLNYCGGQCPH 283  
 OY 284 VAGMPGISAFTHAVNLKANA--AAGTTGRSGCCVPISRRPLSLLYDRDSNIVKTDI 341  
 DB 284 LAGSPGIAASFHSAVSLKANNMPAGS-----SCCVPTARRPLSLLYLDHNGNVKTDV 339  
 OY 342 PDMVVEACGCS 352  
 DB 340 PDMVVEACGCS 350

RESULT 8  
 AAP70200  
 ID AAF70200 standard; protein: 427 AA.

XX AAF70200;

XX 09-APR-1991 (first entry)

XX Sequence of porcine inhibin beta-chain precursor beta-A.

XX Fertility control; contraception; hormone; spermatogenesis.

XX Sus scrofa domestica.

XX

PH Key Location/Qualifiers  
 FT Region 1..308  
 FT Protein /note="used to design a long synthetic DNA probe"  
 FT Cleavage site 309..424  
 FT 304..308  
 FT /note="proteolytic processing site"

XX EF222491-A.

XX 20-MAY-1987.

XX 02-OCT-1986; 86EP-0307586.

XX 12-SEP-1986; 86US-0906729.

XX 03-OCT-1985; 85US-0783910.

XX 10-FEB-1986; 86US-0827710.

XX (GETH ) GENENTECH INC.

XX Mason AJ, Seeburg PH;

XX WPI: 1987-137512/20.

XX N-PSDB; AAN70317.

XX Recombinant human or porcine inhibin or activin - used for  
 PT modulating clinical condition or reproductive physiology of  
 PT animals.

XX Disclosure; Fig 2b; 48pp; English.

A compsn. comprising human or porcine inhibin which is completely  
 CC free of unidentified or porcine proteins is claimed. Also claimed  
 CC are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta  
 CC chain. Sequencing of inhibin-encoding cDNA has led to the  
 CC identification of prodomain regions located N-terminal to the  
 CC mature inhibin chains that represent coordinately expressed  
 CC biologically active polypeptides. The prodomain regions or  
 CC prodomain immunogens are useful in monitoring preproinhibin  
 CC processing in transformant cell culture or in experiments directed  
 CC at modulating the clinical cond. or reproductive physiology of  
 CC animals.

XX Sequence 427 AA:

Query Match 29.8% Score 550.5; DB 8; Length 427;  
 Best Local Similarity 31.6% Pred. No. 1.7e-44;

Matches 133; Conservative 68; Mismatches 143; Indels 77; Gaps 10;

OY 6 LLLALLFTPTTVNPKTEG-----PCPACMGATF--DLSORELLDLAKKSLDKLHLS 58  
 DB 10 LLASCMITVRSPTGSGSHSAAPDCSCALATLPKDVPSOPEMEYAKKHLNMLHLK 69  
 OY 59 QRPILSRVSGALKTALORL-----GPRRETLLEHDQROEYEITSP 102  
 DB 70 KRDPVTCVPKAAALINAIKRLHGVKGVNGVYLEDIDIRRAEM--NELMEGTSILTF 126  
 OY 103 ADTDLSSINOTRLEFHFSGRMASGMEVROTFRMFVOPFH--NATQT--MIRVLY----- 153  
 DB 127 AEAGTAXXKRTLRREISKEGSDLSVERAEITLFLKVKANTRTKVSIRLFQOORRPQ 186  
 OY 154 -----VLRPYDTNLTLTSQYVVOVNASGMYQLLGPBAQAACSGHLLTELVE 202  
 DB 187 GSADAGEAEDVGPFEKESEVLISEKVVDAKSTWHIRPVSSISORLLDQGSALDIRA 246  
 OY 203 SQVAH---SSLILG-----NFSHRPFAVAYR--VEGKH 231  
 DB 247 CEQCHETGASLVLLGKKKKKEEAGRKRDGEGAGVDEEKESHRPPLMLQROSEFHH 306  
 OY 232 RVRRGIDCGGSRMCROEFVDFREIGMNDWIIOPEGYAMNFCGQCPH 291  
 DB 307 FRRRRGLECDGKVNICKKQEFVSKDIGMNDWIILAPSGYHANNYCEGECPSHIACTSGSS 366  
 OY 292 ASFTAVNLKANAAGTGRSGCVPTSRPLSLLYDRDSNIVKTDIPDMVVEACGC 351

DB 367 LSRFSTVYINMTRMGHSHFPAALMKSCCVPTKLRPMMLYDDQDNIIKKIDQNMIVBECG 426

OY 352 S 352

DB 427 S 427

# RESULT 9

AAV92017 standard; Protein: 407 AA.

AC AAV92017;

DT 19-JUL-2000 (first entry)

DE Human inhibin B beta subunit.

KW human inhibin B beta subunit; CKGF; mutant; cysteine knot growth factor; hairpin loop; infertility.

OS Homo sapiens.

Key Location/Qualifiers

FT Misc-difference 1..307 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"

FT Domain 308..328 /label= beta\_hairpin\_loop\_1

FT /note= "mutant optionally comprises one or more substitutions in these residues"

FT Misc-difference 329..375 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"

FT Domain 376..400 /label= beta\_hairpin\_loop\_3

FT /note= "mutant optionally comprises one or more substitutions in these residues"

FT Misc-difference 401..407 /note= "optionally mutated to increase electrostatic interaction between beta hairpin structure and a receptor"

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CC the neurotrophins and the transforming growth factor-beta family; the CC families are known to be structurally similar (especially comprising the CC cysteine knot topology) and it was shown that mutations at certain CC positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological CC activities of the CKGF.

CC Mutant transforming growth factor family proteins or analogues are useful CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained CC infertility, time-limited conception and in assisted reproduction.

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CC the neurotrophins and the transforming growth factor-beta family; the CC families are known to be structurally similar (especially comprising the CC cysteine knot topology) and it was shown that mutations at certain CC positions in the CKGF hairpin loops of family members and other members of the CKGF superfamily could significantly alter the biological CC activities of the CKGF.

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FT Domain 376..400
FT /label= beta_hairpin_loop_3
FT /note= "mutant optionally comprises one or more
FT substitutions in these residues"
FT Misc-difference 401...407
FT /note= "optional mutated to increase electrostatic
FT interaction between beta hairpin structure and
FT a receptor"
PN WO200017360-A1.
PD PD
PD 30-MAR-2000.
XX XX
XX 19-MAR-1999; 99WO-US05908.
PF PF
PR 22-SEP-1998; 98WO-US19772.
PA (UYMA-) UNIV MARYLAND BALTIMORE.
PI Weintraub BD, Szekudlinski MW;
XX XX
XX WPI: 2000-283585/24.
XX XX
PT New mutant cysteine knot growth factor proteins comprising one or more
PT mutant subunits, useful for treating or preventing diseases e.g.
PT hypothyroidism and thyroid cancer
PS PS
PS Claim 328; Page 305; 320pp; English.
XX XX
XX This is the wild type human activin B subunit.
CC Mutants comprise at least one electrostatic charge altering mutation in a
CC beta hairpin loop, resulting in increased bioactivity.
CC CC
CC Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
CC mutant subunits and having novel properties or improved pharmacological
CC properties, compared to wild type CKGFs, are claimed. The CKGF
CC superfamily comprises at least four families of growth factors: the
CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
CC the neurotrophins and the transforming growth factor-beta family; the
CC cystine knot topology) and it was shown that mutations at certain
CC positions in the CKGF hairpin loops of family members and other members
CC of the CKGF superfamily could significantly alter the biological
CC activities of the CKGF.
CC CC
CC Mutant transforming growth factor family proteins or analogues are useful
CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained
CC infertility, time-limited conception and in assisted reproduction.
XX XX
SQ Sequence 407 AA;
Query Match 29.6%; Score 548.5; DB 21; Length 407;
Best Local Similarity 33.3%, Pred. No. 2,4e-44;
Matches 134; Conservative 66; Mismatches 145; Indels 57; Gaps 13
OY 2 ASSLLALLLP-----TPTVVNPKEDEP-----CPACGAIFFDESQREL 42
| | | | | : | | | | | | | | | | | | | | | | | | | |
DB 12 ACULLLAAGCMGLPAMWSPPPTTAAAPPBPSPGSGSDTCTSCGG----FRRPEEL 67
| | | | | : | | | | | | | | | | | | | | | | | | | |
OY 43 -----LIDLAKRSILDLHLTSORPLSLRPSVGALKTALQRLR-GPRRE---TLLEN-- 90
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 68 GRVDGDFLEAVKRIHLSLQMGHRPNITHAIVPKAAVAATLRKLAKGVREGVEIPIHD 127
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 91 -----DQRGEYEITISFADTDLSINOTRLFHFHSGRMASGMEVQTRPMFVO-PFH 142
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 128 GHASPGADCGEVRSEIISFAETDGLASSSRVRLYFLFISNEGONLFVVQASLMYLTKLLPY 187
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 143 ----NMTQTNNIRVLARPDTNLTLTSGYVVYNVASGWQLLGPEAQASOGHTLE 198
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 188 VLEKSGRRKRVRVKVYPOEGHGCDRMNWNEKRDLDKRSNGHTFPFLTEIAQALFEGERGLN 247
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
OY 199 LVPESOVAHSSLIGMF-----SHRPVAAOVRY-EGRHVRVRRGIDCGGSRMCRQE 251
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB 248 LDVQCSCCELAAPVYPVDPGECESHRRPFVVOVALGDSSNRIRIKRGEGCGRNTNCGCO 307
| : | : | : | : | : | : | : | : | : | : | : | : | : | : |

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Oy	252	FVDFREIGNMWMILOPEGYAMNFCQCPHYVGMPGISASFPHAVLNLRKANAA-AGT	310
Dd	308	FFIDFRLGLGNDMIIPTGTGYGNCESSCAPYLGLGVPESSASSFHRAVNQYRMRLNGP	367
Oy	311	TGRSCCVPTSRRPLSLLYDRDSNIYKTDIPDMVEACGS	352
Dd	368	V--NSCCTPTKSTMSMLYFDDEYNIVAKRVPNNIIVECGCA	407
<hr/>			
RESULT 11			
AAP70204	ID	AAP70204 standard; protein; 353 AA.	
XX	AC	AAP70204;	
XX	DT	09-APR-1991 (first entry)	
XX	DE	Sequence of human inhibin beta-chain precursor beta-B.	
XX	KW	Fertility control; contraception; hormone; spermatogenesis.	
XX	OS	Homo sapiens.	
XX	FT	Key	Location/Qualifiers
XX	FT	Modified-site	38..40
XX	FT	Region	/note="potential N-linked glycosylation sites"
XX	FT	Protein	1..237
XX	FT	Cleavage-site	/note="used to design a long synthetic DNA probe"
XX	FT		238..343
XX	FT		235..237
XX	PD	EP222491-A.	/note="proteolytic processing site"
XX	PD	20-MAY-1987.	
XX	XX	02-OCT-1986;	86EP-0307586.
XX	PR	12-SEP-1986;	86US-0906729.
XX	PR	03-OCT-1985;	85US-0783910.
XX	PR	10-FEB-1986;	86US-0827710.
XX	PA	(GETH ) GEMENTECH INC.	
XX	PI	Mason AJ, Seeburg PH;	
XX	DR	WPI, 1987-137512/20.	
XX	DR	N-PSDB; MANN70316.	
XX	PT	Recombinant human or porcine inhibin or activin - used for	
XX	PT	modulating clinical condition or reproductive physiology of	
XX	PT	animals.	
XX	PS	Disclosure; Fig 9A; 48pp; English.	
XX	CC	A compen. comprising human or porcine inhibin which is completely	
XX	CC	free of unidentified or porcine proteins is claimed. Also claimed	
XX	CC	are non chromosomal DNA encoding inhibin-alpha or an inhibin-beta	
XX	CC	chain. Sequencing of inhibin-encoding cDNA has led to the	
XX	CC	identification of prodomain regions located N-terminal to the	
XX	CC	mature inhibin chains that represent coordinately expressed	
XX	CC	biologically active polypeptides. The prodomain regions or	
XX	CC	prodomain immunogens are useful in monitoring preproinhibin	
XX	CC	processing in transformant cell culture or in experiments directed	
XX	CC	at modulating the clinical cond. or reproductive physiology of	
XX	CC	animals.	
XX	SQ	Sequence 353 AA;	
<hr/>			
Query Match	29.4%:	Score 543; DB 8; Length 353;	
Best Local Similarity	34.5%:	Pred. No. 6, 9e-44;	
Matches 124; Conservative	64;	Mismatches 133; Indels 38; Gaps 11;	

OY 26 CPACWCAIFDLESQREL-----LLDLAKSILDKLHLSQRPILSRVSGALTKALQRL 79  
 DB 1 CTRSCG-----FRPEELGRVDCDFLEAVKRRILSRLOMRGRPNTHAVPKAAWYALKKL 56  
 OY 80 R-GPRE-----TLLEH-----DORGEYEIISFADTDLSSINQRLFEHFGSGMASG 126  
 DB 57 HAKGVEDGHEVEIPHLIDHASPGADGERSSEIISFAETDLASRVLVLPISNEGON 116  
 OY 127 MEVRQTFEFMEFVQ-FPH-----NATOTMNIIVLVLRPYDNTLTLSQYVVOVNASGWYOLL 181  
 DB 117 LEVVOASLMLYLKLPLVLEKSGRRKRVKVVYFQEGHGRDMMNVEKRVDLKRSQWHTFP 176  
 OY 182 LCPBQAACSGQHLTLELVPSQVNAHSLIGMF-----SHRPVAAQVRY-EGKHRYR 234  
 DB 177 LTELQALFERGERRLNDVOCDSQELAVVPEVDPGEESHRPVPVVOARLQDSHRIR 236  
 OY 235 RRGIDCGGSRMCCROEFVDFREIGWMDMIIQPEGYAMNFGTGCPLHVAGMPGISASF 294  
 DB 237 KRGLCCGRTMCCROEFFIDRLIGMNDMIIAPGICYGNVEGSGCPALVAGVGSASSF 296  
 OY 295 HTAVNLILKANAA-AGTGRGSCCVPTSRRPLSLLYDRDSNIVKTDIDMVEACGCS 352  
 DB 297 HTAVNOYRMGLNPGTV--NSCCIPTRKLTSMMLYFDEYINIVKRDVPMIVECGCA 353

## RESULT 12

AAF70203  
 ID AAF70203 standard; protein; 426 AA.

AC AAF70203;  
 DT 09-APR-1991 (first entry)  
 DE Sequence of human inhibin beta-chain precursor beta-A.  
 KM Fertility control; contraception; hormone; spermatogenesis.  
 XX Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT Modified-site 165..167  
 FT Region /note="potential N-linked glycosylation sites"  
 FT Region 1..28  
 FT Region /note="signal sequence"  
 FT Region 28..310  
 FT Region /note="pro region"  
 FT Protein 311..326  
 FT Cleavage-site 306..310  
 FT /note="proteolytic processing site"

EP22491-A.

20-MAY-1987.

02-OCT-1986; 86EP-0307586.

12-SEP-1986; 86US-0906729.

03-OCT-1985; 85US-0783910.

10-FEB-1986; 86US-0827710.

(GETH) GENENTECH INC.

Mason AJ, Seeburg PH;

WPI: 1987-137512/20.

N-PSDB; AAN70315.

Recombinant human or porcine inhibin or activin - used for  
modulating clinical condition or reproductive physiology of  
animals.

Disclosure: fig 8A; 48pp; English.

CC A compsn. comprising human or porcine inhibin which is completely  
 CC free of unidentified or porcine proteins is claimed. Also claimed  
 CC are non chromosomal DNA encoding inhibin alpha or an inhibin-beta  
 CC chain. Sequencing of inhibin-encoding cDNA has led to the  
 CC identification of prodomain regions located N-terminal to the  
 CC mature inhibin chains that represent coordinately expressed  
 CC biologically active polypeptides. The prodomain regions or  
 CC prodomain immunogens are useful in monitoring proinhibin  
 CC processing in transformant cell culture or in experiments directed  
 CC at modulating the clinical cond. or reproductive physiology of  
 CC animals.

Sequence 426 AA:

Query Match 29.28; Score 540; DB 8; Length 426;

Best Local Similarity 31.28; Pred. No. 1,76-43; Indels 82; Gaps 11;

Matches 132; Conservative 70; Mismatches 139;

OY 6 LLALEFPTTVVNPRTG-----PCPACWCAIF--DLESQRELLDLAKSILDKLHLS 58  
 DB 10 LLAACWIVRSPPPGSGHSAAPDCSCALALPKDVPNSQPEVNAVKHILNMLHLK 69  
 OY 59 ORPILSRVSGALTKALQRL-----GPRRETLLEHDPQGEYEIISF 102  
 DB 70 KRDPYQVPKRAALLNAIRKLHVKGVEIEDDIGRAEM--NEIMEQTSIITF 126  
 OY 103 ADTDLSSINQRLFEHFGSGMASGMEVROTREMFVQPH-NATOR-MNIRVVLPRY-- 158  
 DB 127 AE--SGTARKTLHEISKEGSDLSVERAEVWLFKVPANTRKVTIRLQOQKHQP 183  
 OY 159 -----DTLLTLTSQYVVOVNASGWYQLLGPBQAACSGQHLTLEL--- 199  
 DB 184 GSLDTGEAEVGLKGERSELLSEKVVADARKSTWIVFPVSSSIQPLDQKSLDVRIA 243  
 OY 200 VPESQVNAHSLIL-----GPFSHRPVAAQVRY--VEG 229  
 DB 244 CECCQSSGASLVLLGKKKKKEEGECKKKGCGACAGADEKEESHRRPFLMLQAROSEDH 303  
 OY 230 KHRVRRRGIDCGGSRMCCROEFVDFREIGWMDMIIQPEGYAMNFGTGCPLHVAGMPG 289  
 DB 304 PHRRRRRGLECDGKVINICCKKQEFVSKDIGWMDMIIAPSGYMANVYEGECPHISG 363  
 OY 290 ISASFHTAVNLILKANAAAGTGRGSCCVPTSRRPLSLLYDRDSNIVKTDIDMVEAC 349  
 DB 364 SLSLFSHTVINHYRMGRSHPPANLSCCVPKLRPMKMLYDDOQNIKKIOMNIVEEC 423  
 OY 350 GCS 352  
 DB 424 GCS 426

## RESULT 13

AAV92016

AAV92016

19-JUL-2000 (first entry)

Human inhibin A beta subunit.

human inhibin A beta subunit; CKGF; mutant; cysteine knot growth factor;

human inhibin A beta subunit; CKGF; mutant; cysteine knot growth factor;

hairpin loop; infertility.

Homo sapiens.

Key Location/Qualifiers

Misc-difference 1..325 /note="optionally mutated to increase electrostatic

interaction between beta hairpin structure and

Domain 326..346 /label="beta\_hairpin\_loop\_1"

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FT FT /note- "mutant optionally comprises one or more
FT FT substitutions in these residues"
FT FT Misc-difference 347..394
FT FT /note- "optionally mutated to increase electrostatic
FT FT interaction between beta hairpin structure and
FT FT a receptor"
FT FT Domain
FT FT 395..419
FT FT /label= beta_hairpin_loop_3
FT FT /note- "mutant optionally comprises one or more
FT FT substitutions in these residues"
FT FT Misc-difference 420..426
FT FT /note- "optionally mutated to increase electrostatic
FT FT interaction between beta hairpin structure and
FT FT a receptor"
FT FT WO200017360-A1.
FT FT 30-MAR-2000.
FT FT 19-MAR-1999; 99WO-US05908.
FT FT 22-SEP-1998; 98WO-US19772.
FT FT (UYMA-) UNIV MARYLAND BALTIMORE.
FT FT Weintraub BD, Szudlinski MW;
FT FT PI
FT FT DR
FT FT XX
FT FT XX
FT FT WPI: 2000-283585/24.
FT FT
FT FT New mutant cysteine knot growth factor proteins comprising one or more
FT FT mutant subunits, useful for treating or preventing diseases e.g.
FT FT hypothyroidism and thyroid cancer
FT FT
FT FT Claim 283; Page 303; 320pp; English.
FT FT
FT FT This is the wild type human inhibin A beta subunit.
FT FT Mutants comprise at least one electrostatic charge altering mutation in a
FT FT beta hairpin loop, resulting in increased bioactivity.
FT FT Mutant cysteine knot growth factor (CKGF) proteins comprising one or more
FT FT mutant subunits and having novel properties or improved pharmacological
FT FT properties, compared to wild type CKGFs, are claimed. The CKGF
FT FT superfamily comprises at least four families of growth factors: the
FT FT glycoprotein hormones, the platelet-derived growth factor (PDGF) family,
FT FT the neurotrophins and the transforming growth factor-beta family; the
FT FT cysteine knot topology and it was shown that mutations at certain
FT FT positions in the CKGF hairpin loops of family members and other members
FT FT of the CKGF superfamily could significantly alter the biological
FT FT activities of the CKGF.
FT FT Mutant transforming growth factor family proteins or analogues are useful
FT FT for treatment of ovulatory dysfunction, luteal phase defect, unexplained
FT FT infertility, time-limited conception and in assisted reproduction.
FT FT
FT FT Sequence 426 AA:
FT FT
FT FT Query Match 29.2%; Score 540; DB 21; Length 426;
FT FT Best Local Similarity 31.2%; Pred. No. 1.7e-43;
FT FT Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;
FT FT
FT FT 6 LLALEFLPTTVVANKTGC-----PCPACGGAIF--DIESQRELLDLAKKSTLDTLHLS 58
FT FT 10 LLAACWIIIVRSPPPGSGCHSAAPDCPCALALPKDYNNSPENVAVKHTLNLMLHLK 69
FT FT 59 QRPILSRVSGALKTALQRLR-----GPRRETLLEHDOEROEVELISF 102
FT FT 70 KRPDVYQPVKPAALLNAIRKLHVGVNGVEYLEDIDIGRAEM--NELMOTSITIF 126
FT FT 103 ADVDLSSINOTRLEFHFSGRMASGMEVROTREFMFPVOPH-NATQT-NMIRVLVLRPY-- 158
FT FT 127 AE--SCTARTLHFESKESGDSLSVVERAEVWLFKVPKANRTKVTIRLFQOQKHQ 183
FT FT 159 -----DTNLTLSQYVVOVNASGMYQLLCPGAQACSGHLELTL--- 199

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DB 184 GSLDTGEAEENGLKGERSELLSEKVDARKSTWHVFPVSSIQRLLDQKSSLDVRIA 243
OY 200 VPEQVAHSSLLI-----GMSHRPPVAQYR--VEG 229
DB 244 CQCQCSGASLYLLGKKKKKEEGEGKKGGGAGADEKEKQSHRPLMLQARQSEDH 303
OY 230 KHRVRRRGIDCGGSRMCCROEFFVDREIGNWDMIIQPEGYAMNPGCTGCPHVGMPG 289
DB 304 PHRRRRRGLECDGKGVNICKKQFVFSFKDIGMDIIRSGIHANVCBEGCPHIACTSG 363
OY 290 ISAPHTAVNLNLKANAAGTGRKSCVPTSRRLPLSLLYDRDSINVKTDIPDMVVEAC 349
DB 364 SLSFHSYVINHYRMKRGSPFANLKSQCVPTKRLRPMWMLYDDQCNILKRDIONMIVEEC 423
OY 350 GCS 352
DB 424 GCS 426

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RESULT 14  
AA92018  
ID AA92018 standard; Protein: 426 AA.  
AC AA92018;  
XX  
DT 19-JUL-2000 (first entry)  
XX  
DE Human activin A subunit.  
XX  
KW human activin A subunit; CKGF; mutant; cysteine knot growth factor;  
KW hairpin loop; infertility.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 1..325  
FT /note- "optionally mutated to increase electrostatic  
FT interaction between beta hairpin structure and  
FT a receptor"  
FT Domain  
FT 326..346  
FT /label= beta\_hairpin\_loop\_1  
FT /note- "mutant optionally comprises one or more  
FT substitutions in these residues"  
FT Misc-difference 347..394  
FT /note- "optionally mutated to increase electrostatic  
FT interaction between beta hairpin structure and  
FT a receptor"  
FT Domain  
FT 395..419  
FT /label= beta\_hairpin\_loop\_3  
FT /note- "mutant optionally comprises one or more  
FT substitutions in these residues"  
FT Misc-difference 420..426  
FT /note- "optionally mutated to increase electrostatic  
FT interaction between beta hairpin structure and  
FT a receptor"  
FT WO200017360-A1.  
FT 30-MAR-2000.  
FT 19-MAR-1999; 99WO-US05908.  
FT 22-SEP-1998; 98WO-US19772.  
FT (UYMA-) UNIV MARYLAND BALTIMORE.  
FT Weintraub BD, Szudlinski MW;  
FT PI  
FT DR  
FT XX  
FT XX  
FT WPI: 2000-283585/24.  
FT  
FT New mutant cysteine knot growth factor proteins comprising one or more  
FT mutant subunits, useful for treating or preventing diseases e.g.  
FT hypothyroidism and thyroid cancer



XX Claim 313; Page 304; 320pp; English.

PS This is the wild type human activin A subunit.  
 CC Mutants comprise at least one electrostatic charge altering mutation in a  
 CC beta hairpin loop, resulting in increased bioactivity.  
 CC Mutant cysteine knot growth factor (CKGF) proteins comprising one or more  
 CC mutant subunits and having novel properties or improved pharmacological  
 CC properties, compared to wild type CKGFs, are claimed. The CKGF family,  
 CC superfamily comprises at least four families of growth factors: the  
 CC glycoprotein hormones, the platelet-derived growth factor (PDGF) family,  
 CC the neurotrophins and the transforming growth factor-beta family; the  
 CC cysteine knot topology) and it was shown that mutations at certain  
 CC positions in the CKGF hairpin loops of family members and other members  
 CC of the CKGF superfamily could significantly alter the biological  
 CC activities of the CKGF.  
 CC Mutant transforming growth factor family proteins or analogues are useful  
 CC for treatment of ovulatory dysfunction, luteal phase defect, unexplained  
 CC infertility, time-limited conception and in assisted reproduction.

CC Sequence 426 AA:

Query Match 29.2%; Score 540; DB 21; Length 426;  
 Best Local Similarity 31.2%; Pred. No. 1.7e-43;  
 Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;

6 LALLFLPTTVVNPKEG-----PCPACGAI--DLESORELLDLAKSILDKLHS 58  
 10 LASCWIIIVSSPTPGSEGHSAAPDCSCALALPKVDVNSQPEVAVKHHILMLHLK 69  
 59 QRPILSRPVSGALKTALQRL-----GPRRETLLEHQROEYEELISF 102  
 70 KRPTVTPVPRKALMLNIRKLHVGVNGEYVEIEDIGRAEM--NELMOTSELTIF 126  
 103 ADTLLSINQRLFEHFGSGMASGMEVROTREFVQPPH-NATOT-MNIRVLVLRPY-- 158  
 127 AE---SGTARKTLHEIISKESDLSVRAEYMLFLKVPKARTRKTVIRLFQOQKHQ 183  
 159 -----DTNLTLSQYVVOVNASGWYQLLGPDAQACSGHILTEL--- 199  
 184 GSLDTGEAEVEYGLKGERSELLSEKVDARKSTWHVFPVSSIQRLDQKSSLDVRIA 243  
 200 VPESQVAHSLL-----GWFSHRPVYAAQVR--VEG 229  
 244 GEQCEGASGLVLLKKKKKEEGEGGEGGAGADEKQSHRPFLMLQAROSEH 303  
 230 KHRVRRGIDCGGSRMCCROEFVDFREIGMNDWIIOPBGYAMNFCGCPPLHVGMPG 289  
 304 PHRRRRRGLECGKVNICKKQEFVSKFDIGMNDWIIAPSGYHANCCEGCPSHIAGTSG 363  
 290 ISASPHAVLNLKANAAGTTGRCSCVPTSRRLSLIYYDRDSNVKTDIDPMVYAC 349  
 364 SLSFHSYVINYRMGHSPFANLKSCVPTKLRPMSMLYDDQONIKKIDQIMYIEEC 423  
 350 GCS 352  
 424 GCS 426

RESULT 15  
 AAR05413  
 ID AAR05413 standard; protein; 426 AA.

AC AAR05413;

XX 27-JUL-1990 (first entry)

XX BUF-3 human differentiation inducing factor gene product.

XX BUF-3; dhfr; dihydrofolic acid reductase; differentiation.

OS Homo sapiens.

XX JP02009388-A.

XX 12-JAN-1990.

XX 08-JUL-1988; 88JP-0170142.

XX 09-MAR-1988; 88JP-0055270.

XX (AJIN) AJINOMOTO KK.

XX WPT: 1990-055348/08.

XX N-PSDB: AA001648.

XX Physiologically active protein prepn.

XX by transforming plasmid having gene coding physiologically

XX active protein and gene of dihydrofolic acid reductase to hamster

XX ovary etc.

XX Example 1: Fig 1; 12pp; Japanese.

XX Gene may be expressed by transforming a dhfr negative strain of CHO cells

XX with an active BUF-3 gene and dhfr carrying vector. BUF-3 gene product

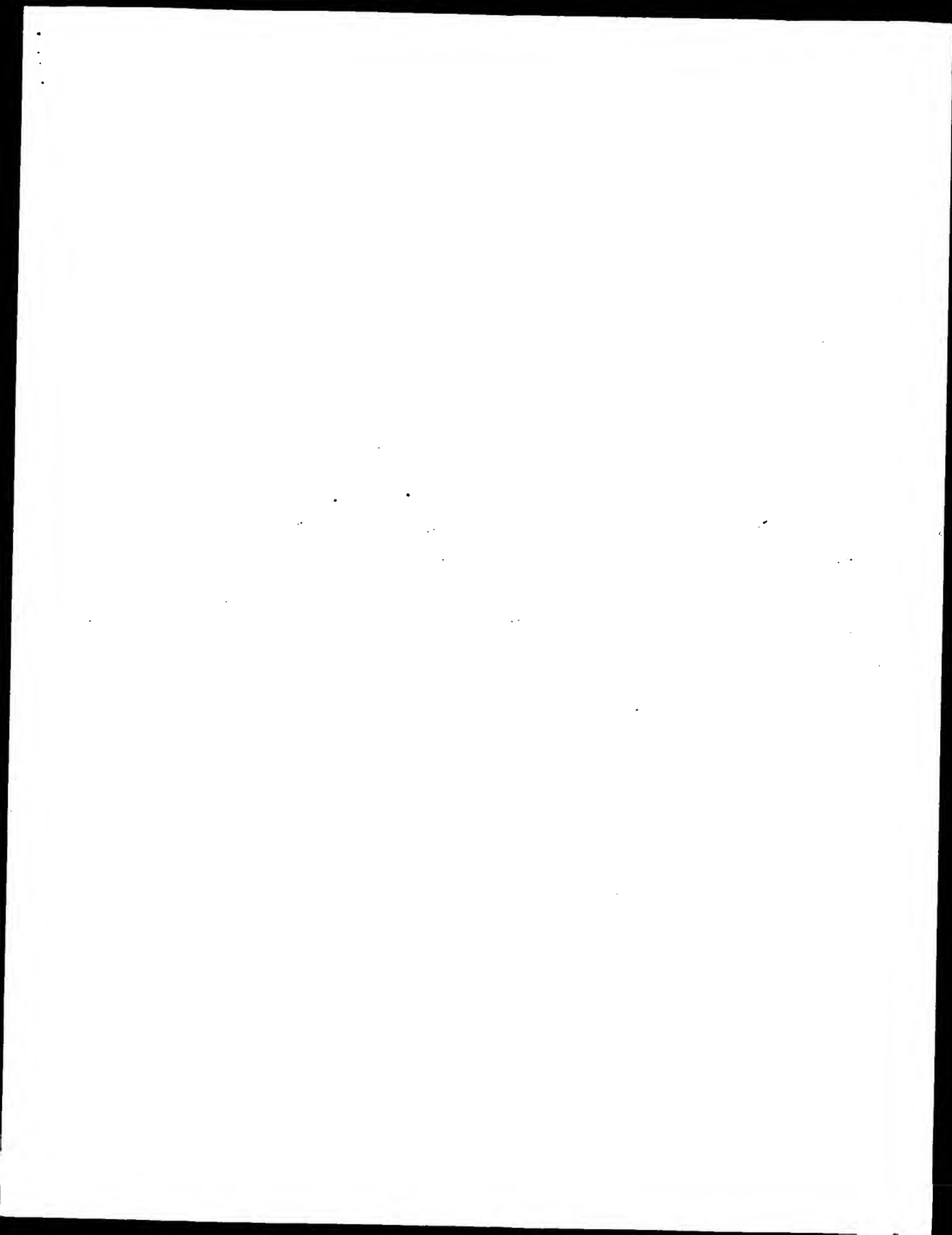
XX is a cell differentiating factor.

Sequence 426 AA:

Query Match 29.1%; Score 538; DB 11; Length 426;  
 Best Local Similarity 31.2%; Pred. No. 2.7e-43;  
 Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;

6 LALLFLPTTVVNPKEG-----PCPACGAI--DLESORELLDLAKSILDKLHS 58  
 10 LASCWIIIVSSPTPGSEGHSAAPDCSCALALPKVDVNSQPEVAVKHHILMLHLK 69  
 59 QRPILSRPVSGALKTALQRL-----GPRRETLLEHQROEYEELISF 102  
 70 KRPTVTPVPRKALMLNIRKLHVGVNGEYVEIEDIGRAEM--NELMOTSELTIF 126  
 103 ADTLLSINQRLFEHFGSGMASGMEVROTREFVQPPH-NATOT-MNIRVLVLRPY-- 158  
 127 AE---SGTARKTLHEIISKESDLSVRAEYMLFLKVPKARTRKTVIRLFQOQKHQ 183  
 159 -----DTNLTLSQYVVOVNASGWYQLLGPDAQACSGHILTEL--- 199  
 184 GSLDTGEAEVEYGLKGERSELLSEKVDARKSTWHVFPVSSIQRLDQKSSLDVRIA 243  
 200 VPESQVAHSLL-----GWFSHRPVYAAQVR--VEG 229  
 244 GEQCEGASGLVLLKKKKKEEGEGGEGGAGADEKQSHRPFLMLQAROSEH 303  
 230 KHRVRRGIDCGGSRMCCROEFVDFREIGMNDWIIOPBGYAMNFCGCPPLHVGMPG 289  
 304 PHRRRRRGLECGKVNICKKQEFVSKFDIGMNDWIIAPSGYHANCCEGCPSHIAGTSG 363  
 290 ISASPHAVLNLKANAAGTTGRCSCVPTSRRLSLIYYDRDSNVKTDIDPMVYAC 349  
 364 SLSFHSYVINYRMGHSPFANLKSCVPTKLRPMSMLYDDQONIKKIDQIMYIEEC 423  
 350 GCS 352  
 424 GCS 426

Search completed: October 12, 2002, 02:06:07  
 Job time : 43 secs



GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: October 12, 2002, 02:05:12 : Search time 15.5 Seconds  
(without alignments)  
554.697 Million cell updates/sec

Title: US-09-684-383-4

Sequence: 1 MSSLALLLELPTTVVNP.....DSNIVKTDIPDMVYACGCCS 352

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

## Database :

1: Issued\_Patents\_AA.\*  
2: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep.\*  
3: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep.\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/1aa/Backfilest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1850	100.0	352	1	US-08-482-577B-4
2	1850	100.0	352	2	US-09-218-176-4
3	1398	75.6	352	1	US-08-482-577B-2
4	1398	75.6	352	3	US-08-289-222E-4
5	1398	75.6	352	4	US-09-218-176-2
6	1398	75.6	352	4	US-09-054-526B-4
7	594	32.1	350	5	PCT-US95-08745-14
8	594	32.1	350	5	US-08-482-577B-24
9	558	30.2	106	3	US-08-289-222E-28
10	558	30.2	106	3	US-08-218-176-7
11	558	30.2	106	4	US-09-054-526B-28
12	546	29.5	349	1	US-08-197-792-33
13	546	29.5	349	1	US-08-459-850-33
14	546	29.5	349	1	US-08-459-850-43
15	543	29.4	353	1	US-08-459-850-43
16	543	29.4	353	1	US-08-197-792-43
17	543	29.4	353	1	US-08-459-850-43
18	543	29.4	353	1	US-08-459-850-43
19	543	29.4	424	1	US-08-197-792-31
20	543	29.4	424	1	US-08-459-850-31
21	543	29.4	424	1	US-08-459-850-31
22	540	29.2	426	1	US-08-197-792-41
23	540	29.2	426	1	US-08-459-850-41
24	540	29.2	426	1	US-08-459-850-41
25	460	24.9	127	1	US-08-455-550-11
26	444	24.0	119	2	US-08-274-215A-12
27	444	24.0	119	2	US-08-765-662-12

28	444	24.0	119	4	US-09-184-933-12	Sequence 12, Appl
29	444	24.0	119	5	PCT-US95-08745-12	Sequence 12, Appl
30	421	22.8	147	4	US-08-065-844A-7	Sequence 7, Appl
31	401.5	21.7	121	1	US-08-581-529B-18	Sequence 18, Appl
32	401.5	21.7	121	1	US-08-455-559-24	Sequence 24, Appl
33	401.5	21.7	121	2	US-08-525-596B-28	Sequence 28, Appl
34	401.5	21.7	121	2	US-08-561-528A-18	Sequence 18, Appl
35	401.5	21.7	121	3	US-09-097-616-18	Sequence 18, Appl
36	401.5	21.7	121	3	US-09-177-860A-28	Sequence 28, Appl
37	401.5	21.7	121	4	US-09-145-060-24	Sequence 24, Appl
38	401.5	21.7	121	5	PCT-US94-00657-24	Sequence 24, Appl
39	401.5	21.7	121	5	PCT-US94-07762-18	Sequence 18, Appl
40	401.5	21.7	121	5	PCT-US94-07799-18	Sequence 18, Appl
41	400.5	21.6	128	1	US-08-455-550-12	Sequence 12, Appl
42	396	21.4	122	1	US-08-581-529B-17	Sequence 17, Appl
43	396	21.4	122	1	US-08-455-559-23	Sequence 23, Appl
44	396	21.4	122	2	US-08-525-596B-27	Sequence 27, Appl
45	396	21.4	122	2	US-08-581-528A-17	Sequence 17, Appl

## ALIGNMENTS

RESULT 1  
US-08-482-577B-4  
Sequence 4, Application US/08482577B  
Patent No. 5807713  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
STREET: SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
PUBLICATION INFORMATION:  
DOCUMENT NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
US-08-482-577B-4  
Query Match 100.0%; Score 1850; DB 1; Length 352;  
Best Local Similarity 100.0%; Pred. No. 1.3e-174;

Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSLLALLFLPTTVNPKTEPCACGCAIFDLESQRELLDLAKSILDKLHSQR 60  
 1 MASSLLALLFLPTTVNPKTEPCACGCAIFDLESQRELLDLAKSILDKLHSQR 60

DB 61 PILSRPVSRGALKTALQRLRGPRRETLLEHDOREYEIISFADTDLSSINOTRLEHFS 120  
 61 PILSRPVSRGALKTALQRLRGPRRETLLEHDOREYEIISFADTDLSSINOTRLEHFS 120

QY 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180  
 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180

DB 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180  
 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180

QY 181 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240  
 181 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240

DB 241 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240  
 241 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240

QY 241 OGGSRMCCROEFFVDREIGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 300  
 241 OGGSRMCCROEFFVDREIGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 300

DB 301 LKANAAGTTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGCS 352  
 301 LKANAAGTTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGCS 352

## RESULT 2

US-09-218-176-4  
 ; Sequence 4, Application US/09218176  
 ; Patent No. 6171584

## GENERAL INFORMATION:

APPLICANT: H TREN, Gertrud  
 APPLICANT: NEIDHARDT, Helge  
 APPLICANT: BECHTOLD, Rolf  
 APPLICANT: POHL, Jens  
 APPLICANT: PAULISTA, Michael  
 TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
 NUMBER OF SEQUENCES: 49  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY & ORAM LLP  
 STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
 CITY: Washington  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/218.176  
 FILING DATE: Herewith  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/679,048  
 FILING DATE: 12-JUL-1996  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP96/03065  
 FILING DATE: 12-JUL-1996  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/EP93/00350  
 FILING DATE: 2-FEB-1993  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 08/482,577  
 FILING DATE: 7-JUN-1995  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 92 102 324.8  
 FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE P 44 23 190.3  
 FILING DATE: 01-JUL-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: DE 195 11 243.1  
 FILING DATE: 27-MAR-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: KITTS, Monica Chln  
 REGISTRATION NUMBER: 36,105  
 REFERENCE/DOCKET NUMBER: P564-6010  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 202/638-5000  
 TELEFAX: 202/638-4810  
 INFORMATION FOR SEQ ID NO: 4:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 352 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-09-218-176-4

Query Match 100.0%; Score 1850; DB 4; Length 352;  
 Best Local Similarity 100.0%; Pred. No. 1.3e-174;  
 Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MASSLLALLFLPTTVNPKTEPCACGCAIFDLESQRELLDLAKSILDKLHSQR 60  
 1 MASSLLALLFLPTTVNPKTEPCACGCAIFDLESQRELLDLAKSILDKLHSQR 60

DB 61 PILSRPVSRGALKTALQRLRGPRRETLLEHDOREYEIISFADTDLSSINOTRLEHFS 120  
 61 PILSRPVSRGALKTALQRLRGPRRETLLEHDOREYEIISFADTDLSSINOTRLEHFS 120

QY 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180  
 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180

DB 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180  
 121 GRMASGMEVROTREFVDFRFGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 180

QY 181 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240  
 181 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240

DB 181 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240  
 181 LIGPEAOAACSOGHLLTELVPESOVAAHSSLLIGWFSHRPFVAAOVRECKHRVRRGIDC 240

QY 241 OGGSRMCCROEFFVDREIGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 300  
 241 OGGSRMCCROEFFVDREIGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 300

DB 241 OGGSRMCCROEFFVDREIGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 300  
 241 OGGSRMCCROEFFVDREIGNDWMIIOPEGYAMNFCGCPPLHVAAGPISASFHTAVLN 300

QY 301 LKANAAGTTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGCS 352  
 301 LKANAAGTTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGCS 352

DB 301 LKANAAGTTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGCS 352  
 301 LKANAAGTTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGCS 352

## RESULT 3

US-08-482-577B-2  
 ; Sequence 2, Application US/08482577B  
 ; Patent No. 5807713

## GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD  
 APPLICANT: NEIDHARDT, HELGE  
 APPLICANT: BECHTOLD, ROLF  
 APPLICANT: POHL, JENS  
 TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
 NUMBER OF SEQUENCES: 49  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: NIKAIKO, MARCELSTEIN, MURRAY, AND ORAM  
 STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY,  
 CITY: WASHINGTON  
 STATE: DC  
 COUNTRY: USA  
 ZIP: 20005  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482,577B  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHARON  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-482-577B-2

Query Match 75.6%; Score 1398; DB 1; Length 352;  
Best Local Similarity 76.2%; Pred. No. 5,6e-130;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFLPTTVVNPKEGPCPCWGAIFDIESRELLDLAKKSILDKLHSOR 60  
DB 1 MTSSLLAFLLAPTTVAIPRAGCCGCPGLESOEELLDLAKKSILDKLHSOR 60  
QY 61 PILSPVSRGALKALQRLRCPRRETLLEHDOQEVEYIISFADTLLSINQRLRPHFS 120  
DB 61 PTLNRPVSRALRTALQHLHGVQGLLE-DNREDECEIISFAGTGLSTINQRLRPHFS 119  
QY 121 G-RMASGMEVROTREMFVQFPNATQTMNIRVLRPYDTNLTLSQYVVOYVNASGWYQ 179  
DB 120 SDRTAGDREVQOASLMFVQLPSNTTWTLKRVLVGPHNTNLTLAQYILLEVDASGMHQ 179  
QY 180 LLLGPEAOAASQGHITLLEVPESQVAHSSLLIGWFSHRPFVAOAVRECKHVRRGID 239  
DB 180 LPLGPEAOAASQGHITLLELVGQVAOSSVILGGAHRRPFVAARVVGKHQHRRGID 239  
QY 240 COGGRMCCROEFVDFRFGIWDWIIQPEGYAMNFCIGCCPLHIAIMPGISASFHTAVL 299  
DB 240 COGGRMCCROEFVDFRFGIWDWIIQPEGYAMNFCIGCCPLHIAIMPGISASFHTAVL 299  
QY 300 NILKANAAGTTGRGSCVPTSRRLPLSLYYDRDSNIVKTDIPDMVEACGCS 352  
DB 300 NILKANTAGTTGGSCCVPTARPLSLYYDRDSNIVKTDIPDMVEACGCS 352

RESULT 4  
US-08-289-222E-4  
Sequence 4, Application US/08289222E  
Patent No. 6120760  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS OF THE TGF-B  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY & ORAM  
STREET: 655 FIFTEENTH STREET, N. W., C STREET LOBBY,  
STREET: SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/289,222E  
FILING DATE: 25-AUG-1999  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 07-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-9021  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-289-222E-4

Query Match 75.6%; Score 1398; DB 3; Length 352;  
Best Local Similarity 76.2%; Pred. No. 5,6e-130;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFLPTTVVNPKEGPCPCWGAIFDIESRELLDLAKKSILDKLHSOR 60  
DB 1 MTSSLLAFLLAPTTVAIPRAGCCGCPGLESOEELLDLAKKSILDKLHSOR 60  
QY 61 PILSPVSRGALKALQRLRCPRRETLLEHDOQEVEYIISFADTLLSINQRLRPHFS 120  
DB 61 PTLNRPVSRALRTALQHLHGVQGLLE-DNREDECEIISFAGTGLSTINQRLRPHFS 119  
QY 121 G-RMASGMEVROTREMFVQFPNATQTMNIRVLRPYDTNLTLSQYVVOYVNASGWYQ 179  
DB 120 SDRTAGDREVQOASLMFVQLPSNTTWTLKRVLVGPHNTNLTLAQYILLEVDASGMHQ 179  
QY 180 LLLGPEAOAASQGHITLLEVPESQVAHSSLLIGWFSHRPFVAOAVRECKHVRRGID 239  
DB 180 LPLGPEAOAASQGHITLLELVGQVAOSSVILGGAHRRPFVAARVVGKHQHRRGID 239  
QY 240 COGGRMCCROEFVDFRFGIWDWIIQPEGYAMNFCIGCCPLHIAIMPGISASFHTAVL 299  
DB 240 COGGRMCCROEFVDFRFGIWDWIIQPEGYAMNFCIGCCPLHIAIMPGISASFHTAVL 299  
QY 300 NILKANAAGTTGRGSCVPTSRRLPLSLYYDRDSNIVKTDIPDMVEACGCS 352  
DB 300 NILKANTAGTTGGSCCVPTARPLSLYYDRDSNIVKTDIPDMVEACGCS 352

RESULT 5  
US-09-218-176-2  
Sequence 2, Application US/09218176  
Patent No. 6171584  
GENERAL INFORMATION:  
APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF

APPLICANT: POHL, Jens  
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
TITLE OF INVENTION: TGF- FAMILY  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., G Street Lobby,  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/218,176  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,048  
FILING DATE: 12-JUL-1996  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03065  
FILING DATE: 12-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 2-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,577  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92 102 324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 11 243.1  
FILING DATE: 27-MAR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTS, Monica Chin  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-6010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-218-176-2

Query Match 75.6% Score 1398; DB 4; Length 352;  
Best Local Similarity 76.2% Pred. No. 5.6e-130;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFLPTTVVNPRTKPCACWCAIFDLESORELLDLAKRSIIDKLHLSOR 60  
DB 1 MTSLLALLFLPTTVVNPRTKPCACWCAIFDLESORELLDLAKRSIIDKLHLSOR 60  
QY 61 PILSRPVSRCALKTALORLGRPRETTLEHDOROEEYIISFADYDLSINOTRLEHPS 120  
DB 61 PTINRPVSRAALRTVALOHIGHVPGALLE-DNRECECETISAEYGLSTINOTRLEHPS 119  
QY 121 G-NWASGMEVROTFRNFVCPHNAOTMTNIRVLVLRPYDNLITLSQYVVOVNASGWYO 179

DB 120 SDRTAGDREYQASLMFVYVLPSTTWTILKRVVLVLPHTNNTLALQYLLVAVASGHWQ 179  
QY 180 LILGPEAOAASQGHLLTLEVPESQVAHSSLLIGWFSHPPEVAQVRECKHRRRCID 239  
DB 180 LILGPEAOAASQGHLLTLEVPESQVAHSSLLIGWFSHPPEVAQVRECKHRRRCID 239  
QY 240 COGSRMCCROEFVDFREIGMNDWITIOPEGYAMNFCGCPPLHVAAMPISASFHTAVL 299  
DB 240 COGSRMCCROEFVDFREIGMNDWITIOPEGYAMNFCGCPPLHVAAMPISASFHTAVL 299  
QY 300 NLKANAAGTTGRGSCCVPTSRPLSLLYDRDSNIVKTDIDPMVVEACGCS 352  
DB 300 NLKANAAGTTGRGSCCVPTSRPLSLLYDRDSNIVKTDIDPMVVEACGCS 352

RESULT 6  
US-09-054-526B-4  
Sequence 4, Application US/09054526B  
Patent No. 6197550  
GENERAL INFORMATION:  
APPLICANT: H TITEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAI, MARMELSTEIN, MURRAY & ORAM LLP  
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054,526B  
FILING DATE: 03-APR-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-8005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 352 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-054-526B-4

Query Match 75.6% Score 1398; DB 4; Length 352;

Best Local Similarity 76.2%; Pred. No. 5.6e-130;  
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

QY 1 MASSLLALLFTPTVYNPKTEGPCACGAIIDLESORELLDLAKKSLDKLHLSOR 60  
1 MTSSLALFLAIPATVPBRAGCCGACGPTLEESQRELLDLAKKSLDKLHLSOR 60  
QY 61 PILSRPRAALALORLGRPRETLEHDOREVEYIISFADPDSINOTRLEFHS 120  
61 PTLNRPVSRALRALALHGVPOGALLE-DNRQDECEIISFAEGLISTINTRLDPFHS 119  
QY 121 G-MASGEMRQTRPFMEFPPHATOTMINIRVLRPYDNLTLTSQVYVYVNSGMWQ 179  
120 SDRTAGDREYQASLMEFVQLPSMTWTLKRVLYLGPHTNLTLATQYLLLEVDASGMWQ 179  
QY 180 LLLEPQAQASQGHLLLELPESQVASHSLILGWFSHRPEVAQVREKGRVRRGID 239  
180 LPLCPQAQASQGHLLLELPESQVASHSLILGWFSHRPEVAQVREKGRVRRGID 239  
QY 240 CQGGSRMCQOEFFVDFREIGWMDMIIQPEGYAMNFCGQPLHAGMPCGISASPHAVL 299  
240 CQGGSRMCQOEFFVDFREIGWMDMIIQPEGYAMNFCGQPLHAGMPCGISASPHAVL 299  
QY 300 NLKANAAGTTGSGCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGS 352  
300 NLKANAAGTTGSGCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGS 352

RESULT 7  
US-08-765-662-14  
Sequence 14, Application US/08765662  
Patent No. 5929213

## GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/765,662

FILING DATE: 28-APR-1997

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042W01 (PD-3830)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:  
US-08-765-662-14

Query Match 32.1%; Score 594; DB 2; Length 350;  
Best Local Similarity 39.3%; Pred. No. 1.3e-50;  
Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;

QY 22 TEGPCACGAIIDLESORELLDLAKKSLDKLHLSORPLSRVSGALALORL- 80  
22 TGSVCBSGGSKLAPOERLALVELAKOIIDGLHLSRPRITRPPRALTRALRRIQ- 81  
QY 81 ---GPRRETLLEHDOREVEYIISFAD-TDLSINOTRLEFHFSGRMASGEVROTREFM 136  
82 GSVAPNGE-----EVSIFATVDTSTAVSSLTTHLS--TRSHHLYARALM 128  
QY 137 FVQPPHATOTMNI-----RVLYLRPYDNLTLTSQVYVYVNSGMWQLLGP 184  
129 HVLPTLPGTCLRIFRMGRRRRROGSRLLAEHHTNL-----GMHTLTPS 175  
QY 185 EAQQAQSGHLLLELPESQVASHSL-----LLGWFSH-RPVAQVRE--GKHVRR 235  
176 SGLRGEKSGYLKLDLDRPLEGNSTVTGOPRRLLDTAGHOQFLFKIRANEPGAGRMR 235  
QY 236 RGIDCQGGSRMCQOEFFVDFREIGWMDMIIQPEGYAMNFCGQPLHAGMPCGISASPH 295  
236 RPTCEPATPCCRHDYVDQELGMDMIIQPEGYAMNFCGQPLHAGMPCGISASPH 295  
QY 296 TAVNLKANA--AAGTTGSGCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGS 352  
296 SAVFSLKANNPFAST-----SCVPTARRPLSLLYDRDSNIVKTDIPDMVVEACGS 350

## RESULT 8

PCT-US95-08745-14  
Sequence 14, Application PC/TUS9508745

## GENERAL INFORMATION:

APPLICANT: THE JOHNS HOPKINS UNIVERSITY SCHOOL OF MEDICINE  
TITLE OF INVENTION: GROWTH DIFFERENTIATION FACTOR-12  
NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson  
STREET: 4225 Executive Square, Suite 1400  
CITY: La Jolla  
STATE: CA  
COUNTRY: USA  
ZIP: 92037

COMPUTER TYPE: Diskette

COMPUTER READABLE FORM:

MEDIUM TYPE: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/08745

FILING DATE: 12-JUL-1995

ATTORNEY/AGENT INFORMATION:

NAME: Hallie, Ph.D., Lisa A

REGISTRATION NUMBER: 38,347

REFERENCE/DOCKET NUMBER: 07265/042W01 (PD-3830)

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619-678-5070

TELEFAX: 619-678-5099

TELEX:

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:

LENGTH: 350 amino acids

TYPE: amino acids

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal



ORIGINAL SOURCE;  
PCT-US95-08745-14

Query Match	32.1%	Score 594;	DB 5;	Length 350;
Best Local Similarity	39.3%	Pred. No. 1.3e-50;		
Matches 141;	Conservative 51;	Mismatches 109;	Indels 58;	Gaps 11;

```

QY      22  TEGPCACGCAIIDLDSQRELLDLAKSIIDLTLSORPLTSRPSRGLKTAALRLR-  80
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      22  TGSVCPSCGGSKLAPQARLALVLELAQOILDDGLHTLSRPTTHPPQALTRALRLQ  81
      81  ---GPRRRTLLEHDOROEYEIISFAD-TDLSSIOTRLEFIHFSGMASGMEYQTRFMF  138
      82  GSVARNGE-----EVISFATVTDSTAVSSLLTFILS--TPRSHLHYHARLML  128
QY      137  FVQGFHNATOTMNI-----RVLYLRPYDNTLTTSQVYVQVNASGMYQELLGP  184
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      129  HVLPLPLGTCLCLIFRMGPRRRRSGRTLLAEHNITNL-----GHNITLTPS  175
QY      185  EAQAACSGCHLTLELVPESQVAASSL-----ILGWFSH-RPVAAQVAVE--GKIRVRR  235
      176  SGLRGEKSSVYLKQLDCCRPLGEGNSTVYGOPRRLLDPTACHOQPLFLKLTIRANEPGACGRAR  235
Db      236  RCIDCGGSRMCCROEPVDFRRELGWMDWIIQREPGYANNFCTGCGPLHVAAGPGIASFH  295
      236  RPTPECPATPLCCRRHHYVDFQELGMDWMILOPBGYQIANTYSGDQPPHLGSGIGIAASFH  295
QY      296  TAVNLMLKANA--AGGTTGSCGSCVPTSRRLSLIYYRDSNVITVDTPDMVVEAGCS  352
      1  : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      296  SAVFSLKANNWPAST-----SCCVPLARRPLSLIYIDHNGVYATVDTPDMVVEAGCS  350

```

RESULT 9  
US-08-48

Sequence 24, Application US/08482577B  
Patent No. 5807713

GENERAL INFORMATION:

APPLICANT: HOTTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS

TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: NIKALDO, MARCELSTEIN, MURRAY, AND ORAM  
STREET: 655 FIFTEENTH STREET, N.W., G STREET LOBBY  
CITY: WASHINGTON  
STATE: DC

COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patengin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/482.577B  
FILING DATE:

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: KLESNER, SHAWN  
REGISTRATION NUMBER: 36,335  
REFERENCE/DOCKET NUMBER: P564-5010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

```

;      TOPOLOGY: linear
;      MOLECULE TYPE: peptide
US-08-482-577B-24

```

Query Match	30.2%	Score 558	DB 1	Length 106
Best Local Similarity	93.4%	Pred. No.	8.6e-48	
Matches	99	Conservative	4	Mismatches 3
				Indels 0
				Gaps 0

[illegible]

RESULT 10  
US-08-289

```

Sequence 28, Application US/08289222E
Patent No. 6120760

GENERAL INFORMATION:
APPLICANT: HOTTEN, GERTTRUD
APPLICANT: ALDENHARDT, HELGE
APPLICANT: BECHTOLD, ROLF
APPLICANT: POHL, JENS
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTOR
TITLE OF INVENTION: FAMILY
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORA
STREET: 655 FIFTEENTH STREET, N. W., G STREET
STREET: SUITE 310
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-5701

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/289,222E
FILING DATE: 25-AUG-1999

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/289,222
FILING DATE: 12-AUG-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 44 23 190.3
FILING DATE: 07-JUL-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EPO 92102324.8
FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP93/00350
FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:
NAME: KITTS, MONICA CHIN
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: P564-9021
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/638-5000
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear

MOLECULE TYPE: protein
5S-08-289-222E-28

```

Query Match 30.2% Score 558; DB 3; Length 106;  
Best Local Similarity 93.4%; Pred. No. 8.6e-48;  
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 247 CCRQEFFVDEREIGMNDWIIQPEGYAMNFCIGCCPLHAGMPGISASHTAVLNLLKANA 306  
DB 1 CCRQEFFVDEREIGMNDWIIQPEGYAMNFCIGCCPLHAGMPGISASHTAVLNLLKANT 60

OY 307 AAGTTGGSCCVPTRRPLSLIYYDRDSNIVKTDIPDMVVEACGS 352  
DB 61 AAGTTGGSCCVPTRRPLSLIYYDRDSNIVKTDIPDMVVEACGS 106

RESULT 11  
US-09-218-176-7  
Sequence 7, Application US/09218176

GENERAL INFORMATION:  
PATENT NO. 6171584  
APPLICANT: H TTEN, Gertrud  
APPLICANT: NEIDHARDT, Helge  
APPLICANT: BECHTOLD, Rolf  
APPLICANT: POHL, Jens  
APPLICANT: PAULISTA, Michael  
TITLE OF INVENTION: NEW GROWTH/DIFFERENTIATION FACTORS OF THE  
TITLE OF INVENTION: TGF- FAMILY  
NUMBER OF SEQUENCES: 49  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 Fifteenth Street, N. W., G Street Lobby,  
STREET: Suite 330  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/218.176  
FILING DATE: Herewith

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/679,048  
FILING DATE: 12-JUL-1996

CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/03065  
FILING DATE: 12-JUL-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 2-FEB-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/482,577  
FILING DATE: 7-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EP 92 102 324.8  
FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 195 11 243.1  
FILING DATE: 27-MAR-1995

ATTORNEY/AGENT INFORMATION:  
NAME: KITTIS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-6010  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein

US-09-218-176-7

Query Match 30.2% Score 558; DB 4; Length 106;  
Best Local Similarity 93.4%; Pred. No. 8.6e-48;  
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 247 CCRQEFFVDEREIGMNDWIIQPEGYAMNFCIGCCPLHAGMPGISASHTAVLNLLKANA 306  
DB 1 CCRQEFFVDEREIGMNDWIIQPEGYAMNFCIGCCPLHAGMPGISASHTAVLNLLKANT 60

OY 307 AAGTTGGSCCVPTRRPLSLIYYDRDSNIVKTDIPDMVVEACGS 352  
DB 61 AAGTTGGSCCVPTRRPLSLIYYDRDSNIVKTDIPDMVVEACGS 106

RESULT 12  
US-09-054-526B-28  
Sequence 28, Application US/09054526B

GENERAL INFORMATION:  
PATENT NO. 6197550  
APPLICANT: H TTEN, GERTRUD  
APPLICANT: NEIDHARDT, HELGE  
APPLICANT: BECHTOLD, ROLF  
APPLICANT: POHL, JENS  
TITLE OF INVENTION: DNA SEQUENCES ENCODING NOVEL  
TITLE OF INVENTION: GROWTH/DIFFERENTIATION FACTORS  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: NIKAIIDO, MARCELSTEIN, MURRAY & ORAM LLP  
STREET: 655 FIFTEENTH STREET, N. W., G STREET LOBBY,  
STREET: SUITE 330  
CITY: WASHINGTON  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-5701

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/054.526B  
FILING DATE: 03-APR-1998

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/289,222  
FILING DATE: 12-AUG-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE P 44 23 190.3  
FILING DATE: 01-JUL-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: EPO 92102324.8  
FILING DATE: 12-FEB-1992

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP93/00350  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: KITTIS, MONICA CHIN  
REGISTRATION NUMBER: 36,105  
REFERENCE/DOCKET NUMBER: P564-8005  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202/638-5000  
TELEFAX: 202/638-4810

INFORMATION FOR SEQ ID NO: 28:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 106 amino acids  
TYPE: amino acid

STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
us-09-054-5268-28

Query Match 30.28; Score 558; DB 4; Length 106;  
Best Local Similarity 93.48; Pred. No. 8,66-48;  
Matches 99; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 247 CCGDEPVDREIGMNMIIPEGYANMCTGCGCPHYAGMPGISASFTAVLNLKANA 306  
|||||  
DB 1 CCGDEPVDREIGMNMIIPEGYANMCTGCGCPHYAGMPGISASFTAVLNLKANA 60

QY 307 AACGTGSCCVPTSRRLSLYYDRDSNIYKTDIPDMVVEACGCS 352  
|||||  
DB 61 AACGTGSCCVPTSRRLSLYYDRDSNIYKTDIPDMVVEACGCS 106

## RESULT 13

US-08-197-792-33  
Sequence 33, Application US/08197792

Patent No. 5525488

GENERAL INFORMATION:

APPLICANT: Anthony J. Mason

APPLICANT: Peter H. Seeburg

TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or Beta Chains of Inhibin and

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/197,792

FILING DATE: 16-FEB-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/958414

FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744207

FILING DATE: 12-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/215466

FILING DATE: 05-JUL-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/906729

FILING DATE: 31-DEC-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/827710

FILING DATE: 07-FEB-1986

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/783910

FILING DATE: 03-OCT-1985

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: 297P2D4

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415/225-1896

TELEFAX: 415/952-9881

TELEX: 910/371-7168

INFORMATION FOR SEQ ID NO: 33:

SEQUENCE CHARACTERISTICS:

LENGTH: 349 amino acids

TYPE: amino acid

TOPOLOGY: linear  
US-08-197-792-33

Query Match 29.5%; Score 546; DB 1; Length 349;  
Best Local Similarity 35.88; Pred. No. 7,1e-46;  
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

QY 44 LDLAKSILDKLHLSRPIISRPVSGALKTALQRLR-GPRE--TLER----- 90  
|||  
DB 17 LEAVKRHLINRLQMRGPNITHAVPKAAWYALRLKLAGKREGRVETIPLDGHASGA 76

QY 91 DQKQEEYIIISFADTILSNQTRLEFESGRMASGMEVQTRPMFVQ-FPH---NAT 145  
|||  
DB 77 DQKQEEYIIISFADTILSNQTRLEFESGRMASGMEVQTRPMFVQ-FPH---NAT 136

QY 146 QTRNIRVLYRPYDTNLTLSQYVQVYAGWQVLLGPEQAQCSGHLTLEVPESQV 205  
|||  
DB 137 RYRVVYVYQEPHGHGMDVVEKRVDLKRGWMTLPLEAIOALFERGERLNDVOCDC 196

QY 206 AHSLLIGWF-----SHREVAQVAV-EGKRRVRRGIDCGSRMCCROEFFVDFRE 258  
|||  
DB 197 CQELAVPVYVDFGESHREFVYVQARLGDSSRRIRKRGLECDRTVLCRQOFFIDRL 256

QY 259 IGMNDMIIPEGYANMCTGCGCPHYAGMPGISASFTAVLNLKANA-AGTGRGSCC 317  
|||  
DB 257 IGMNDMIIPEGYANMCTGCGCPHYAGMPGISASFTAVLNLKANA-AGTGRGSCC 314

QY 318 VPTSRRLSLYYDRDSNIYKTDIPDMVVEACGCS 352  
|||  
DB 315 IPTKLSMTSMLYFDDENYIVKROVPMNIVEECGA 349

## RESULT 14

US-08-459-850-33

Sequence 33, Application US/08459850

Patent No. 5665568

GENERAL INFORMATION:

APPLICANT: Anthony J. Mason

APPLICANT: Peter H. Seeburg

TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or

TITLE OF INVENTION: Beta Chains of Inhibin and Method for synthesizing Polypept

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 460 Point San Bruno Blvd

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/459,850

FILING DATE: 02-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/197792

FILING DATE: 17-FEB-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/958414

FILING DATE: 08-OCT-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/744207

FILING DATE: 12-AUG-1991

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/215466

FILING DATE: 05-JUL-1988

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 06/906729

FILING DATE: 31-DEC-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/827710  
FILING DATE: 07-FEB-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/783910  
FILING DATE: 03-OCT-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 297P2D5  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ. ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 349 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-459-850-33

Query Match 29.5% Score 546; DB 1; Length 349;  
Best Local Similarity 35.8%; Pred. No. 7.1e-46;  
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

QY 44 LDKAKSIIDKHLISORPILSRGALKTALORLR-GPRE---TLEH----- 90  
DB 17 LEAVKRIILNRLOKRGPRNTHAVPKAMVTLAKLHAGKVEDGVEIPIHLDGHSAPGA 76  
QY 91 DOROEYEIISFADTDLSSINOTRLEFHSGRMASGMEVROTFRMFVQ-FPH---NAT 145  
DB 77 DGERVSEIISFATDGLASSRVRLYFISNNGNOLFVQASLMYLKLLPVLKESGR 136  
QY 146 QTNIRIVLRYPTDNLTLTSQYVQVNASGYOLLGPEAAGSCGHLTELVPESQV 205  
DB 137 RKRVKRVYFQEPGCHDRMDVVEKRYDLKRSCHWHTLPLEAIALFGRGRLMLDVQCDG 196  
QY 206 AHSSLLIGWF-----SHRPVAAQVRV-EKGRVRRRGIDCGGSMCCROEFPVDFRE 258  
DB 197 COELAVPVFVDPCEESHRPVPVQARLDSDSRIRKRLGLEDGCRNLCCROQOFFIDRL 256  
QY 259 IGNNDWIIOPGYAMNCTGOCPLHVGMPGISASFHTAVNLKLNAA-AGTTGRSGSC 317  
DB 257 IGSMDWIIAPGYGNGCEGSPALVAGVPGSASSFHTAVNQRMRGLNPGTV--NSCC 314  
QY 318 VPTSRPRLSLYYDRDSNIVKTDIPDMVVEACGCS 352  
DB 315 IPTKLTSMMLYFDDEVNIVKRDVPMIIVECGCA 349

RESULT 15  
US-08-459-214-33  
Sequence 33, Application US/08459214  
Patent No. 5716810  
GENERAL INFORMATION:  
APPLICANT: Anthony J. Mason  
APPLICANT: Peter H. Seeburg  
TITLE OF INVENTION: Nucleic Acid Encoding the Alpha or  
TITLE OF INVENTION: Beta Chains of Inhibin and Method for Synthesizing Polypeptide  
TITLE OF INVENTION: using such Nucleic Acid  
NUMBER OF SEQUENCES: 44  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: patln (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/459, 214  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/197792  
FILING DATE: 17-FEB-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/958414  
FILING DATE: 08-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/744207  
FILING DATE: 12-AUG-1991  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/215466  
FILING DATE: 05-JUL-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/906729  
FILING DATE: 31-DEC-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/827710  
FILING DATE: 07-FEB-1986  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 06/783910  
FILING DATE: 03-OCT-1985  
ATTORNEY/AGENT INFORMATION:  
NAME: Hasak, Janet E.  
REGISTRATION NUMBER: 28,616  
REFERENCE/DOCKET NUMBER: 297P2D6  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1896  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ. ID NO: 33:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 349 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-459-214-33

Query Match 29.5% Score 546; DB 1; Length 349;  
Best Local Similarity 35.8%; Pred. No. 7.1e-46;  
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

QY 44 LDKAKSIIDKHLISORPILSRGALKTALORLR-GPRE---TLEH----- 90  
DB 17 LEAVKRIILNRLOKRGPRNTHAVPKAMVTLAKLHAGKVEDGVEIPIHLDGHSAPGA 76  
QY 91 DOROEYEIISFADTDLSSINOTRLEFHSGRMASGMEVROTFRMFVQ-FPH---NAT 145  
DB 77 DGERVSEIISFATDGLASSRVRLYFISNNGNOLFVQASLMYLKLLPVLKESGR 136  
QY 146 QTNIRIVLRYPTDNLTLTSQYVQVNASGYOLLGPEAAGSCGHLTELVPESQV 205  
DB 137 RKRVKRVYFQEPGCHDRMDVVEKRYDLKRSCHWHTLPLEAIALFGRGRLMLDVQCDG 196  
QY 206 AHSSLLIGWF-----SHRPVAAQVRV-EKGRVRRRGIDCGGSMCCROEFPVDFRE 258  
DB 197 COELAVPVFVDPCEESHRPVPVQARLDSDSRIRKRLGLEDGCRNLCCROQOFFIDRL 256  
QY 259 IGNNDWIIOPGYAMNCTGOCPLHVGMPGISASFHTAVNLKLNAA-AGTTGRSGSC 317  
DB 257 IGSMDWIIAPGYGNGCEGSPALVAGVPGSASSFHTAVNQRMRGLNPGTV--NSCC 314  
QY 318 VPTSRPRLSLYYDRDSNIVKTDIPDMVVEACGCS 352  
DB 315 IPTKLTSMMLYFDDEVNIVKRDVPMIIVECGCA 349

Search completed: October 12, 2002, 02:10:49  
Job time : 16.5 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 12, 2002, 01:13:12 : Search time 27 seconds  
(without alignments)  
1252.720 Million cell updates/sec

Title: us-09-684-383-4

Perfect score: 1850  
Sequence: 1 MASSLLALLFLPTTVVNP.....DSNIVKTDIPDMVVEACGCS 352

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: PIR1:\*  
2: PIR2:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1850	100.0	352	2 JC5366	activin beta C - m
2	1844	99.7	352	2 S70580	activin beta C pre
3	1398	75.6	352	2 JC2466	inhibin beta-C cha
4	699.5	37.8	367	2 JC4151	activin beta D cha
5	581.5	31.4	350	2 JC5241	activin beta E cha
6	566.5	30.6	370	2 I51199	activin beta B sub
7	551	29.8	408	2 S50899	activin beta B prec
8	549.5	29.7	411	2 B41398	inhibin beta-B cha
9	548.5	29.6	407	2 A40150	inhibin beta-B cha
10	546	29.5	349	1 WEPGBB	inhibin beta-A cha
11	543	29.4	424	1 WEPGBA	inhibin beta-A cha
12	540	29.2	426	1 B24288	inhibin beta-A cha
13	538	29.1	424	1 S31440	inhibin beta-B - z
14	533.5	28.8	393	2 I50103	inhibin beta-A cha
15	532.5	28.8	425	1 S50898	inhibin beta-A cha
16	529.5	28.6	425	2 I47072	inhibin beta-A cha
17	529	28.6	424	1 B40905	activin beta-A cha
18	528	28.6	413	2 JC4862	activin beta-A cha
19	456	24.5	255	2 I48235	inhibin beta-B cha
20	356	19.2	115	2 PNO506	activin beta B-1 c
21	353	19.1	115	2 PNO505	activin beta B-2 c
22	330	17.8	115	2 C36192	activin beta-B2 cha
23	312.5	16.9	101	2 B36192	inhibin beta-A cha
24	311.5	16.8	101	2 A36192	inhibin beta-B cha
25	292	15.8	102	2 A36192	activin - fruit fl
26	283.5	15.3	373	2 PM0042	bone morphogenetic
27	273	14.8	396	1 BMH02	bone morphogenetic
28	261.5	14.1	393	2 S37073	bone morphogenetic
29	257	13.9	394	2 S45355	bone morphogenetic

30	252.5	13.6	372	2 C39364	GDF-1 embryonic gr
31	252.5	13.6	401	2 JH0689	bone morphogenetic
32	249.5	13.5	400	2 A49147	bone morphogenetic
33	249	13.5	357	2 A39364	GDF-1 embryonic gr
34	248	13.4	454	1 BMH05	bone morphogenetic
35	246	13.3	402	2 A45056	osteogenic protein
36	244.5	13.2	353	2 I50607	bone morphogenetic
37	244.5	13.2	510	2 A54798	Vg-1-related prote
38	243.5	13.2	408	2 S58791	bone morphogenetic
39	243.5	13.2	513	1 BMH06	bone morphogenetic
40	243	13.1	398	2 JH0688	bone morphogenetic
41	243	13.1	398	2 JH0687	bone morphogenetic
42	241.5	13.1	365	2 T43286	act-1 protein - Ca
43	239	12.9	452	2 I49542	bone morphogenetic
44	238.5	12.9	313	2 I51284	bone morphogenetic
45	235.5	12.7	426	2 JH0690	bone morphogenetic

## ALIGNMENTS

## RESULT 1

activin beta C - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 28-May-1997 #sequence\_revision 18-Jul-1997 #text\_change 26-Aug-1999  
C:Accession: JC5366  
R:Fang, J.; Wang, S.; Smiley, E.; Bonadio, J.  
Biochem. Biophys. Res. Commun. 231, 655-661, 1997  
A:Title: Genes coding for mouse activin beta C and beta E are closely linked and exhi  
A:Reference number: JC5366; MUID:97224404  
A:Accession: JC5366  
A:Molecule type: DNA  
A:Residues: 1-352 <FAN>  
A:Cross-references: GB:U95962  
C:Comment: Activin beta C and beta E form a distinct subset of related activins.  
C:Genetics:  
A:Introns: 105/3  
C:Superfamily: Inhibin

Query Match 100.0%; Score 1850; DB 2; Length 352;  
Best Local Similarity 100.0%; Pred. No. 7.6e-162;  
Matches 352; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MASSLLALLFLPTTVVNPKEGPCACWGAIFDLESQRELLDLAKKSLDKLHLSQR 60	
DB	1	MASSLLALLFLPTTVVNPKEGPCACWGAIFDLESQRELLDLAKKSLDKLHLSQR 60	
OY	61	PIISRPVSRGALKTALORLGRPRETLLHDDQROEEYELISFADTDLSSINOTRUEHFS 120	
DB	61	PIISRPVSRGALKTALORLGRPRETLLHDDQROEEYELISFADTDLSSINOTRUEHFS 120	
OY	121	GRNASGMEVAVQTRFMFVOPPHNATOTMNIRVLVRYDNTLITTSOVVYVNASGWTOL 180	
DB	121	GRNASGMEVAVQTRFMFVOPPHNATOTMNIRVLVRYDNTLITTSOVVYVNASGWTOL 180	
OY	181	LLGPPEAOACSGCHLTLELPESQVAAHSSLLIGFSSHPFVAAGVREKGRHVRRGIDC 240	
DB	181	LLGPPEAOACSGCHLTLELPESQVAAHSSLLIGFSSHPFVAAGVREKGRHVRRGIDC 240	
OY	241	QGSRRMCROEFVDFREIGNNDWIIOPEGYAMNECTQCCLHVAAGMGISAFITAVLN 300	
DB	241	QGSRRMCROEFVDFREIGNNDWIIOPEGYAMNECTQCCLHVAAGMGISAFITAVLN 300	
OY	301	LLKNAAGTGGRCSCVPTSRRLSLILYDRDSNIVTIDIPDMVVEACGCS 352	
DB	301	LLKNAAGTGGRCSCVPTSRRLSLILYDRDSNIVTIDIPDMVVEACGCS 352	

## RESULT 2

S70580  
activin beta C precursor - mouse  
C:Species: Mus musculus (house mouse)

C>Date: 14-Feb-1997 #sequence\_revision 13-Mar-1997 #text\_change 26-Aug-1999  
 C/Accession: S70580  
 R/Lau, A.L.; Nishimori, K.; Matzuk, M.M.  
 Biochim. Biophys. Acta 1307, 145-148, 1996  
 A>Title: Structural analysis of the mouse activin beta-C gene.  
 A/Reference number: S70580; MUID:96283807  
 A/Accession: S70580  
 A/Status: Preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-352 <LAU>  
 A/Cross-references: EMBL:U40772  
 C/Genetics:  
 A/Introns: 106/1  
 C/Superfamily: Inhibin

Query Match  
 Best Local Similarity 99.78; Score 1844; DB 2; Length 352;  
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MASSLLALFLPTTVVNPKEGPCACGALFDESORELLDLAKKSLDKLHLSOR 60  
 DB 1 MASSLLALFLPTTVVNPKEGPCACGALFDESORELLDLAKKSLDKLHLSOR 60  
 OY 61 PILSRPVSGALKTALQRLGPRRETLLHDQROEEYEIISFADTDLSSINOTLREHFS 120  
 DB 61 PILSRPVSGALKTALQRLGPRRETLLHDQROEEYEIISFADTDLSSINOTLREHFS 120  
 OY 121 GNASGMEVROTRPFMFVOPPHNATQTMNIRVLVLRPYDTNLTLSQYVQVNASGWYOL 180  
 DB 121 GNASGMEVROTRPFMFVOPPHNATQTMNIRVLVLRPYDTNLTLSQYVQVNASGWYOL 180  
 OY 181 LILGPEAOAASOGHLLTLELVPESOVAHSSLILGMSHRRPVAOVREKHNRRRGIDC 240  
 DB 181 LILGPEAOAASOGHLLTLELVPESOVAHSSLILGMSHRRPVAOVREKHNRRRGIDC 240  
 OY 241 OGGSMCCROEFFVDREIGNMDWIIQPEGYAMNCTGOCPLHVAGMPISASFHTAVLN 300  
 DB 241 OGGSMCCROEFFVDREIGNMDWIIQPEGYAMNCTGOCPLHVAGMPISASFHTAVLN 300  
 OY 301 LILKANAAGTTGGSCCVPFTRRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352  
 DB 301 LILKANAAGTTGGSCCVPFTRRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352

## RESULT 3

JC2466  
 Inhibin beta-C chain precursor - human  
 N/Alternate names: activin beta C chain  
 C/Species: Homo sapiens (man)  
 C/Date: 29-Mar-1995 #sequence\_revision 26-May-1995 #text\_change 29-Oct-1999  
 C/Accession: JC2466  
 R/Hoetton, G.; Neidhardt, H.; Schneider, C.; Pohl, J.  
 Biochem. Biophys. Res. Commun. 206, 608-613, 1995  
 A>Title: Cloning of a new member of the TGF-beta family: A putative new activin betaC ch  
 A/Reference number: JC2466; MUID:95126961  
 A/Accession: JC2466  
 A/Molecule type: mRNA  
 A/Residues: 1-352 <HOE>  
 A/Cross-references: GB:X82540; NID:9669154; PIDN:CAA57890.1; PID:9669155  
 A/Experimental source: Liver  
 C/Genetics:  
 A/Genes: GDB:INHBC  
 A/Cross-references: GDB:632884  
 A/Map position: 2cen-2q13  
 C/Superfamily: Inhibin  
 C/Keywords: glycoprotein  
 F:1-18/Domain: signal sequence #status predicted <SIG>  
 F:19-236/Domain: signal sequence #status predicted <PRO>  
 F:237-352/Product: activin beta C #status predicted <MAT>  
 F:110,143,161/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match  
 Best Local Similarity 75.6%; Score 1398; DB 2; Length 352;  
 Matches 351; Conservative 76.2%; Pred. No. 2,3e-120;

Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

OY 1 MASSLLALFLPTTVVNPKEGPCACGALFDESORELLDLAKKSLDKLHLSOR 60  
 DB 1 MASSLLALFLPTTVVNPKEGPCACGALFDESORELLDLAKKSLDKLHLSOR 60  
 OY 61 PILSRPVSGALKTALQRLGPRRETLLHDQROEEYEIISFADTDLSSINOTLREHFS 120  
 DB 61 PILSRPVSGALKTALQRLGPRRETLLHDQROEEYEIISFADTDLSSINOTLREHFS 120  
 OY 121 G-RMASGMEVROTRPFMFVOPPHNATQTMNIRVLVLRPYDTNLTLSQYVQVNASGWYOL 179  
 DB 121 G-RMASGMEVROTRPFMFVOPPHNATQTMNIRVLVLRPYDTNLTLSQYVQVNASGWYOL 179  
 OY 180 LILGPEAOAASOGHLLTLELVPESOVAHSSLILGMSHRRPVAOVREKHNRRRGIDC 239  
 DB 180 LILGPEAOAASOGHLLTLELVPESOVAHSSLILGMSHRRPVAOVREKHNRRRGIDC 239  
 OY 240 COGSMCCROEFFVDREIGNMDWIIQPEGYAMNCTGOCPLHVAGMPISASFHTAVLN 299  
 DB 240 COGSMCCROEFFVDREIGNMDWIIQPEGYAMNCTGOCPLHVAGMPISASFHTAVLN 299  
 OY 300 LILKANAAGTTGGSCCVPFTRRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352  
 DB 300 LILKANAAGTTGGSCCVPFTRRPLSLYYDRDSNIVKTDIDPMVVEACGCS 352

## RESULT 4

JC4151  
 activin beta D chain precursor - African clawed frog  
 C/Species: Xenopus laevis (African clawed frog)  
 C/Date: 27-Aug-1995 #sequence\_revision 19-Oct-1995 #text\_change 21-Jul-2000  
 C/Accession: JC4151  
 R/Oda, S.; Nishimatsu, S.; Murakami, K.; Ueno, N.  
 Biochem. Biophys. Res. Commun. 210, 581-588, 1995  
 A>Title: Molecular cloning and functional analysis of a new activin beta subunit: a d  
 A/Reference number: JC4151; MUID:95275314  
 A/Accession: JC4151  
 A/Molecule type: mRNA  
 A/Residues: 1-367 <ODA>  
 A/Cross-references: DDB:J49543; NID:9661512; PIDN:BA08494.1; PID:9661513  
 A/Experimental source: embryo  
 C/Superfamily: Inhibin  
 C/Keywords: glycoprotein; mesoderm  
 F:1-253/Domain: signal sequence #status predicted <SIG>  
 F:254-367/Product: activin beta D chain #status predicted <MAT>  
 F:64,155,161,208,230/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match  
 Best Local Similarity 37.8%; Score 699.5; DB 2; Length 367;  
 Matches 145; Conservative 65; Mismatches 122; Indels 37; Gaps 7;

OY 6 LIALFLPTTVVNPKEGPCACGALFDESORELLDLAKKSLDKLHLSOR 65  
 DB 14 LILTLALASTOGILTKKSCPCSCG-----VQKEVYIELAKQIILOKLHKERPNITH 67  
 OY 66 PVSRGALKTALOR--LKGPRRETL-----ENDQROEEYEIISFADTDLSSINOT 113  
 DB 66 PVSRGALKTALOR--LKGPRRETL-----ENDQROEEYEIISFADTDLSSINOT 113  
 OY 114 RLEFHSGRMASGMEVROTRPFMFVOPPHNATQTMNIRVLVLRPYDTNLTLSQYVQVNASGWYOL 173  
 DB 128 TLFQFTTRKESQSAHVLAHLMLEPFKANRTSQONETRLVLYOAVSRRLISERKLEPR 187  
 OY 174 ASGWYOLLLGPEAOAASOGHLLTLELVPESOVAHSSLILGMSHRRPVAOVREKHNRRRGIDC 224  
 DB 188 WTGMQRFESLKSMLQTFPFGDNKSLQLELNDGQDQVYVLANPNN-----SHQPFVLAQ 240  
 OY 225 VAV--EKKHRRRRRGIDCQGGSMCCROEFFVDREIGNMDWIIQPEGYAMNCTGOCPLHVAGMPISASFHTAVLN 283  
 DB 241 ARVHDSHATKRSKLNCDQNSNLCKRKYVYVDFKIDGMNMIILKPEYQYINCYGGLCPMH 300  
 OY 284 VAGMPISASFHTAVLNILKANAAGTTGGSCCVPFTRRPLSLYYDRDSNIVKTDIDP 343





```

OY 76 LQRLR-GPRRE---TLLEH-----DQROEYEIISFADTDLSSINQRLFEHFSGR 122
DB 108 LRLHAKGVREDGVEIPLHLDGHSFGADGQERSEIISFETDGLASSRVLKLPFI 167
OY 123 MASGMEYRQTRFMEFVQFPHNAQTMINIIVLVPRYDNTLTSQYV-----VQYNASGW 177
DB 168 GNQNLFLVQAQSLMYLTKLPLVLEKGRKRVKRVYVQEGQPGDRMAVEKRVLDKRGW 227
OY 178 YQULLPEQAQASQGHULTLELPESQVHSSLLGMF-----SHRPFVAQVRV-EGK 230
DB 228 HTPPLTEPIQALFSGRGRRLSLDVOCDSCRELAVVPVFDGESHREPFVVAQRLGDSR 287
OY 231 HVRVRGIDQCGSRMCCROEFVDFREIGNDMIIOEGYAMNFCGCPCLHVAQMGI 290
DB 288 HIRKRGLEDGDRNTNLCCROGFFIDFLICNDMIIPATGYGNYCEGSCPAVLGVPGS 347
OY 291 SASFHTAVLNLKANA-ACTTGRGSCCVPTSRRLSLLYDRDSNIYKTDIPKMYVAC 349
DB 348 ASSFHTAVVQYHMRGLNPGTV--NSCCIPTKLSTMVLTVDDEYNTYKRDVPMNIVEEC 405
OY 350 GCS 352
DB 406 GCA 408

```

## RESULT 8

B41398

Inhibin beta-B chain precursor - rat

M:Alternate names: Inhibin/activin beta B-chain

C:Species: Rattus norvegicus (Norway rat)

C:Date: 03-Apr-1992 #sequence, revision 01-Aug-1997 #text\_change 16-Jul-1999

C:Accession: B41398; #3288; C40905

R:Feng, Z.M.; Li, Y.P.; Chen, C.L.C.

Mol. Endocrinol. 3, 1914-1925, 1989

A:Title: Analysis of the 5'-flanking regions of rat inhibin alpha- and beta-B-subunit g

A:Reference number: A41398; MUID:90190649

A:Accession: B41398

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-174 &lt;FEN&gt;

A:Cross-references: GB:M32756; GB:M32757; MID:9204943; PIDN:AAA41438.1; PID:9554460

R:Dykema, J.C.; Mayo, K.E.

Endocrinology 135, 702-711, 1994

A:Title: Two messenger ribonucleic acids encoding the common beta B-chain of inhibin and

A:Reference number: 153288; MUID:94307180

A:Accession: 153288

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-7 &lt;RES&gt;

A:Cross-references: GB:S72477; MID:9619268

R:Esch, F.S.; Shimasaki, S.; Cooksey, K.; Mercado, M.; Mason, A.J.; Ying, S.Y.; Ueno, N.

Mol. Endocrinol. 1, 388-396, 1987

A:Title: Complementary deoxyribonucleic acid (cDNA) cloning and DNA sequence analysis of

A:Reference number: A40905; MUID:90331931

A:Accession: C40905

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: mRNA

A:Residues: 133-411 &lt;ESC&gt;

C:Superfamily: Inhibin

```

Query Match          29.7%  Score 549.5; DB 2:  Length 411;
Best Local Similarity 32.8%  Pred. No. 2e-42;
Matches 134; Conservative 67; Mismatches 142; Indels 65; Gaps 12;
OY 2 ASLLALLFL-----PPTVVNPKTEGP-----CPACWKALPDLSEREL 42
DB 12 ACULLLAGWGLPEAMGSTRPPSPRAAPP PPPPAPGSGDTCSCGGGGGFRREPEL 71
OY 43 -----LIDLAKKSLDKLHLSQRPILSRVSGALKTALQRLR-GPRRE---TLLEH-- 90
DB 72 GRVDDFLFAVVRHILSRQLGRPNITHAVPKAMVNTLRLKIHAKGVREDGVEIPLHD 131
OY 91 -----DQROEYEIISFADTDLSSINQRLFEHFSGMASGMEYRQTRFMEFVQ-FPH 142

```

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DB 132 GHASPADQQERSEIISFETDGLASSRVLKLPFIFFVNEGQNLFLVQAQSLMYLTKL 191
OY 143 ----NATOTWINIVLVLRPVDNTLTSQYVVOYNASGWQOLLGPEQAQASQGHULTLE 198
DB 192 VLEKGRKRVKRVYVQEGQPGDRMAVEKRVLDKRGWHTFTEAIIQALFEGERLN 251
OY 199 LPVESQVHSSLLGMF-----SHRPFVAQVRV-EGKHRVRGIDQCGSRMCCROE 251
DB 252 LDVQDCSCQELAVVPVFDGESHREPFVVAQRLGDSRRIRKRGLEDGDRNTNLCCROQ 311
OY 252 FVDFREIGNDMIIOEGYAMNFCGCPCLHVAQMGISASFTAVLNLKANAAGTT 311
DB 312 FFDRLIIGNDMIIPATGYGNYCEGSCPAVLGVPGASASFTAVVNOYRM----- 364
OY 312 GRG-----SCCVPTSRRLSLYDRDSNIYKTDIPDWNVEACGS 352
DB 365 -RGIANPYNNSCIPTKLSMSMLTFDDEYNTYKRDVPMNIVEECGCA 411

```

## RESULT 9

A40150

Inhibin beta-B chain precursor - human

M:Alternate names: activin AB chain B

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text\_change 01-Dec-2000

C:Accession: A40150; C24248; A40156; S10751

R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.

Biochem. Biophys. Res. Commun. 135, 957-964, 1986

A:Title: Structure of two human ovarian inhibins.

A:Reference number: A90123; MUID:86186863

A:Accession: C24248

A:Molecule type: mRNA

A:Residues: 53-407 &lt;MA2&gt;

A:Cross-references: GB:M13437; MID:9186416; PIDN:AAA59169.1; PID:9186417

R:Feng, Z.M.; Bardin, C.W.; Chen, C.L.C.

Mol. Endocrinol. 3, 939-948, 1989

A:Title: Characterization and regulation of testicular inhibin beta-subunit mRNA.

A:Reference number: A40156; MUID:89293443

A:Accession: A40156

A:Molecule type: mRNA

A:Residues: 22-46, 'A', '48-407 &lt;FEN&gt;

A:Cross-references: GB:M1632

R:Schmeizler, C.H.; Burton, L.E.; Timony, C.M.; Schwall, R.H.; Mason, A.J.; Liegeois,

Bloodim. Biophys. Acta 1039, 135-141, 1990

A:Title: Purification and characterization of recombinant human activin B.

A:Reference number: S10751; MUID:90304183

A:Accession: S10751

A:Molecule type: Protein

A:Residues: 293-294, 'GX', 297-302, 'XX', 305-307 &lt;SCH&gt;

A:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respec

bin beta-A and beta-B, respectively.

C:Genetics:

A:Gene: GDB:INHBR

A:Cross-references: GDB:119347; OMIM:147390

A:Map position: 2cen-2q13

C:Superfamily: Inhibin

C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone

F:1-20/Domain: signal sequence #status predicted &lt;SIG&gt;

F:21-292/Domain: propeptide #status predicted &lt;PRO&gt;

F:293/Product: inhibin beta-B chain #status predicted &lt;MAT&gt;

F:93/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.6% Score 548.5; DB 1: Length 407;

Best Local Similarity 33.3%; Pred. No. 2.5e-42;  
Matches 134; Conservative 66; Mismatches 145; Indels 57; Gaps 13;

QY 2 ASLLALLALL-----TPTTVNPKTEG-----CPACNKAIFDLESREL 42  
DB 12 ACILLALLAAGMCPBAMKSPPTPPAPPPPPSPGSGODTCTSCG---FRPEEL 67  
QY 43 -----LDDAKKSLDKLHLSORPLSRPVSGALKTALQRLR-GPRRE---TLEH-- 90  
DB 68 GRVDGDFLEAVKRIILSRQKGRPNITHAVPKAAVTLAKRLHAKKVRDGEVEIPLD 127  
QY 91 -----DOROEYEIISFADTDLSSINQTRLEFHSGMASGMEVROTFRMFVQ-FPH 142  
DB 128 GHASPGADGQERSEIISFADTDLSSINQTRLEFHSGMASGMEVROTFRMFVQ-FPH 187  
QY 143 -----NATOTMINIRLVLPYDTNLTLSQYVQVNAAGYOLLGPDAACSGHLLTLE 198  
DB 188 VLEKSGRRKRYKRVYFQDQCHDRMNNVEKRYDLKRSQHITPLTALQALFERGERLN 247  
QY 199 LVPESSQVAHSLILGMF-----SHRPVAAQVRV-EGKHRRARRGIDCGGSRMCCROE 251  
DB 248 LDVQCSQCELAIVPVFVDPGESESHRPVAAQVRVQARLDSRRHRIKRGLECDGRTNLCCROQ 307  
QY 252 FVDFREIGNNDWITIOPEGYAMNCTGOCPLHVGMPGISASPHAVNLKANA-AQT 310  
DB 308 FFDIFRLIGNDWITIAIPGYIGNCEGSCPAYLAGPSSASSPHAVNOYRMKGLMPGT 367  
QY 311 TGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACGS 352  
DB 368 V--NSCCIPTKLSTMSMLYFDEYNIIVKRDVPMIIVECGCA 407

## RESULT 10

MEPGBA  
Inhibin beta-B chain precursor - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 30-Jun-1987 #sequence\_revision 30-Jun-1987 #text\_change 01-Dec-2000  
C:Accession: A01394  
R:Maeson, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Veno, N.; Ying, S.Y.; Gullemin, R.;  
Nature 318, 659-663, 1985  
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precursor  
A:Reference number: A93371; MUID:86092207  
A:Accession: A01394  
A:Molecule type: mRNA  
A:Residues: 1-349 <MAS>  
A:Cross-references: GB:X03267; NID:g2005; PIDN:CAA27020.1; PID:g2006  
C:Comment: The source of this protein is ovarian follicular fluid.  
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypeptide  
different forms of inhibin have been isolated (A and B) that differ in the amino-terminal  
C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of follicle  
stimulating hormone.  
C:Superfamily: Inhibin  
C:Keywords: contraceptive; follicle tropin inhibitor; glycoprotein; gonadotropin releasing  
hormone; propeptide (fragment) #status predicted <PRO>  
F:1-234/Domain: propeptide (fragment) #status predicted <PRO>  
F:235-349/Product: inhibin beta-B chain (covalent) #status predicted  
F:35/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.5%; Score 546; DB 1; Length 349;  
Best Local Similarity 35.8%; Pred. No. 3.4e-42;  
Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9;

QY 44 LDDAKKSLDKLHLSORPLSRPVSGALKTALQRLR-GPRRE---TLEH----- 90  
DB 17 LEAVKRIILSRQKGRPNITHAVPKAAVTLAKRLHAKKVRDGEVEIPLDGHASPA 76  
QY 91 DOROEYEIISFADTDLSSINQTRLEFHSGMASGMEVROTFRMFVQ-FPH-----NAT 145  
DB 77 DQGERVEIISFADTDLSSINQTRLEFHSGMASGMEVROTFRMFVQ-FPH-----NAT 145  
QY 146 QTMIRLVLPYDTNLTLSQYVQVNAAGYOLLGPDAACSGHLLTLEIPESSOV 205  
DB 137 RAVRVKRYFQDQCHDRMNNVEKRYDLKRSQHITPLTALQALFERGERLNLDVQCDG 196  
QY 206 AHSLLILGMF-----SHRPVAAQVRV-EGKHRRARRGIDCGGSRMCCROE FVDFRE 258

DB 197 COELAVPVFVDPGESESHRPVAAQVRVQARLDSRRHRIKRGLECDGRTNLCCROQ FIDFL 256

QY 259 IGMNDWITIOPEGYAMNCTGOCPLHVGMPGISASPHAVNLKANA-ACTTGRGSCC 317

DB 257 IGMSDWITIAIPGYIGNCEGSCPAYLAGPSSASSPHAVNOYRMKGLMPGT--NSCC 314

QY 318 VPTSRRLSLLYDRDSNIVKTDIPDMVVEACGS 352

DB 315 IFTKLTMSMLYFDEYNIIVKRDVPMIIVECGCA 349

## RESULT 11

MEPGBA  
Inhibin beta-A chain precursor - pig  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 13-Aug-1986 #sequence\_revision 13-Aug-1986 #text\_change 18-Jun-1999  
C:Accession: A01393  
R:Maeson, A.J.; Hayflick, J.S.; Ling, N.; Esch, F.; Veno, N.; Ying, S.Y.; Gullemin, R.;  
Nature 318, 659-663, 1985  
A:Title: Complementary DNA sequences of ovarian follicular fluid inhibin show precurs  
A:Reference number: A93371; MUID:86092207  
A:Accession: A01393  
A:Molecule type: mRNA  
A:Residues: 1-424 <MAS>  
A:Cross-references: GB:X03266; NID:g2002; PIDN:CAA27020.1; PID:g2003  
C:Comment: The source of this protein is ovarian follicular fluid.  
C:Comment: The mature protein is the carboxyl-terminal segment of a precursor polypep  
different forms of inhibin have been isolated (A and B) that differ in the amino-termi  
C:Comment: Inhibin is secreted by ovaries or testes and inhibits the secretion of fol  
stimulating hormone.  
C:Superfamily: Inhibin  
C:Keywords: contraceptive; follicle tropin inhibitor; glycoprotein; gonadotropin releasing  
hormone; propeptide (fragment) #status predicted <PRO>  
F:1-20/Domain: signal sequence #status predicted <SIG>  
F:21-308/Domain: propeptide #status predicted <PRO>  
F:309-424/Product: inhibin beta-A chain (covalent) #status predicted  
F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 29.4%; Score 543; DB 1; Length 424;  
Best Local Similarity 31.6%; Pred. No. 8.4e-42;  
Matches 133; Conservative 67; Mismatches 141; Indels 80; Gaps 11;

QY 6 LIALFLPTTVNPKTEG-----CPACNKAIF--DLESORELLDLAKSLDKLHLS 58  
DB 10 LIAACWIIYVSSPTPGSGHSAAPDCSCALATLPKDVNPNGPENVAVKRIILNLHLK 69  
QY 59 QRPILSRPVSGALKTALQRLR-----GPRRETLLEHDOOEYEIISF 102  
DB 70 KRPDQVOPVKAALNLKRIHVGKVGENGVELEDIGRAEM--NELMOTSEIITF 126  
QY 103 ADTDLSSINQTRLEFHSGMASGMEVROTFRMFVQFPH-NATOT-MNIRVL----- 153  
DB 127 AEAGTA---RKTIRFELSKSGSDLSYVERAEIWLKVPKANRTKVSIRIFQOORRPQ 183  
QY 154 -----VLRYDTNLTLSQYVQVNAAGYOLLGPDAACSGHLLTLEIPE 202  
DB 184 GSADAGEBAEDVGFPEEKSEYLLSEKVVADARKSTWHTIPPVSSIORLLDQGSALDIRTA 243  
QY 203 SOVAH-----SSILIG-----WFSHRPFAVQVR--VEGRH 231  
DB 244 CQCHETGASLVLLKKKKKEEFAEGKRKROEGAGVDEKQSHRPFLMLQAROSEH 303  
QY 232 RVRRRGIDCGGSRMCCROE FVDFREIGNNDWITIOPEGYAMNCTGOCPLHVGMPGIS 291  
DB 304 RRRRRGLECDGKVNICKKQFVSKDIGNDWITIAIPGYHANYCEGEPHIAAGTSGS 363  
QY 292 ASFHTAVNLKANAAGTGRGSCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACCC 351  
DB 364 LSFHSTVINYRMKRGSPFANLASCVPPTKLRPMISMLYDDGQNIIRKIDQIMMIVEECG 423  
QY 352 S 352  
DB 424 S 424

## RESULT 12

B24248

Inhibin beta-A chain precursor (validated) - human

N:Alternate names: activin A; activin AB chain A; erythroid differentiation factor; mega

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 08-Dec-2000

C:Accession: S30488; B23556; B24248; S33351; P00010

R:Tanimoto, K.; Handa, S.I.; Ueno, N.; Murakami, K.; Fukumizu, A.

DNA Seq. 2, 103-110, 1991

A:Title: Structure and sequence analysis of the human activin beta(A) subunit gene.

A:Reference number: S30488; MUID:92135888

A:Accession: S30488

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-426 &lt;MAN&gt;

A:Cross-references: EMBL:X57578; NID:928351; PIDN:CAA0805.1; PID:9835621

A:Note: the authors translated the codon GAG for residue 53 as Gly and GAG for residue 5

R:Stewart, A.G.; Milborrow, H.M.; Ring, J.M.; Crowther, C.E.; Forage, R.G.

FEBS Lett. 206, 329-334, 1986

A:Title: Human inhibin genes. Genomic characterisation and sequencing.

A:Reference number: A91366; MUID:87005283

A:Accession: B23556

A:Molecule type: DNA

A:Residues: 311-426 &lt;STED&gt;

A:Cross-references: GB:X04447; NID:933928; PIDN:CAA28041.1; PID:933929

R:Mason, A.J.; Niall, H.D.; Seeburg, P.H.

Biochem. Biophys. Res. Commun. 135, 957-964, 1986

A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the inh

A:Reference number: A30884; MUID:88190086

A:Accession: A30884

A:Molecule type: mRNA

A:Residues: 1-426 &lt;MAS&gt;

A:Cross-references: GB:M13436; NID:9186414; PIDN:AAA59168.1; PID:9307069

R:Murata, M.; Eto, Y.; Shibata, H.; Sakai, M.; Muramatsu, M.

Proc. Natl. Acad. Sci. U.S.A. 85, 2434-2438, 1988

A:Title: Erythroid differentiation factor is encoded by the same mRNA as that of the inh

A:Reference number: A30884; MUID:88190086

A:Accession: A30884

A:Molecule type: mRNA

A:Residues: 1-426 &lt;MUR&gt;

A:Cross-references: GB:J03634; NID:9181946; PIDN:AAA35787.1; PID:9181947

R:Berry, H.; Walter, M.; Northemann, W.

submitted to the EMBL Data Library, April 1993

A:Description: Nucleotide sequence coding for the mature subunit beta(A) of human inhib

A:Reference number: S33351

A:Accession: S33351

A:Molecule type: preliminary

A:Residues: 311-426 &lt;BER&gt;

A:Cross-references: EMBL:X72498; NID:9297786; PIDN:CAA51163.1; PID:9755740

R:Fujimoto, K.; Kawakita, M.; Kato, K.; Yonemura, Y.; Masuda, T.; Matsuzaki, H.; Hirose,

Biochem. Biophys. Res. Commun. 174, 1163-1168, 1991

A:Title: Purification of megakaryocyte differentiation activity from a human fibrous his

A:Reference number: P00010; MUID:91144591

A:Accession: P00010

A:Molecule type: protein

A:Residues: 311-313, 'X', 315-320, 'XX', 323-328, 'X', 330-334 &lt;FUJ&gt;

C:Comment: Activins A and B are homodimers of inhibin beta-A or inhibin beta-B, respecti

bin beta-A and beta-B, respectively.

C:Genetics:

A:Gene: GDB:11N8A

A:Cross-references: GDB:119346; OMIM:147290

A:Map position: 7p15-7p13

A:Introns: 129/3

C:Superfamily: inhibin

C:Keywords: glycoprotein; gonad; heterodimer; homodimer; hormone

F:1-28/Domain: signal sequence #status predicted &lt;STG&gt;

F:29-310/Domain: propeptide #status predicted &lt;PRO&gt;

F:311-426/Product: inhibin beta A chain #status experimental &lt;MAT&gt;

F:165/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match : 29.28; Score 540; DB 1; Length 426;

Best Local Similarity 31.2%; Pred. No. 1,6e-41;

Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;

QY 6 LLALLFLPTTYVNVNKTET-----PCPACGALF--DLSEORELLDLAKSLDKLHL 58

DB 10 LLASCIWIIVRSSPTGSEBHSAPDPCALALPKDVPSPQEPMEVAKKHLIMLTK 69

QY 59 QRPITSRVSRCALKTALORL-----GPRRETLHDROEYEISF 102

DB 70 KRPDYTOPVPKALINAIKLLHVGKGVGEYVEIEDDGRABE---NELMEQSEITTF 126

QY 103 ADTDLSSINQRLERFHFSGRMAAGMEVQRTREMFVQFPH-NATQT-MNIRVVLRLPY-- 158

DB 127 AE--SGTARKLHFEISKEGSDLSVERAEVWLPKVPANRRITVTRLPQOKHPQ 183

QY 159 -----DTNLTLSQYVVOVMASGWQLLGPQAACSGHLEL--- 199

DB 184 GSLDTGEAEVGLKGERSELLSEKVDARKSTWHVFPVSSIQRLDQKSLDVIA 243

QY 200 VPESQVANSLL-----GMSHNPFAVAOVR--VEG 229

DB 244 CEQCEGASLVLLGKKKKKEEGEGGKGEGGAGADEKEQSHRPFLMQARQSDH 303

QY 230 KHRVRRGRTDQCGSRMCCROEFVDFREIWNMDIIPRGYAMNPTGCPHVAHMPG 289

DB 304 PHRRRRKLECDGKVNICKQFVFSKIDGMDWIIIPSGYANVCEGECSPHATGSG 363

QY 290 ISAPFTAVLNILKNAAGTGRGSCCVPTSRPLSLTYDRDSNVTKTDIPMVVEAC 349

DB 364 SLSHSHVYINHYRARGHSPANLKSCTPTKLRPMMLTYDDQNIKKDIONMYDEC 423

QY 350 GCS 352

DB 424 GCS 426

## RESULT 13

S31440

Inhibin beta-A chain - mouse

N:Alternate names: activin A; mesoderm-inducing factor WEHI-MIF

C:Species: Mus musculus (house mouse)

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 10-Sep-1999

C:Accession: A60087; I48265; S31440

R:Albano, R.M.; Gotsdave, S.F.; Huylbroeck, D.; Van Nimmen, K.; Isaacs, H.V.; Slack,

Development 110, 435-443, 1990

A:Title: A mesoderm-inducing factor produced by WEHI-3 murine myelomonocytic leukemia

A:Reference number: A60087; MUID:92155098

A:Accession: A60087

A:Molecule type: protein

A:Residues: 309-311, 'X', 313-318, 'XX', 321-325 &lt;AL2&gt;

R:Albano, R.M.; Groome, N.; Smith, J.C.

Development 117, 711-723, 1993

A:Title: Activins are expressed in preimplantation mouse embryos and in ES and EC cel

A:Reference number: I48243; MUID:93321614

A:Accession: I48265

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-424 &lt;RES&gt;

A:Cross-references: EMBL:X69619; NID:950145; PIDN:CAA49325.1; PID:950146

C:Superfamily: inhibin

Query Match : 29.1%; Score 538; DB 1; Length 424;

Best Local Similarity 32.1%; Pred. No. 2,4e-41;

Matches 136; Conservative 68; Mismatches 134; Indels 86; Gaps 14;

QY 6 LLALLFLPTTYVNVNKTET-----PCPACGALFDL-----ESQRELLDLAKSLDKL 55

DB 10 LLASCIWIIVRSSPTGSEBHSAPDPCALALPKDVPSPQEPMEVAKKHLIMLTK 66

QY 56 HLSQRTISRPSRCALKTALORL-----GPRRETLHDROEYEI 99

DB 67 HLKRPDYTOPVPKALINAIKLLHVGKGVGEYVEIEDDGRABE---NELMEQSEI 123



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OY 200 VPESQVAHSSLIL-----GMFSHRPFAVAOVR--VECK 230
DB 244 CECCQETGASLVLLGKKKKKEEGBGKKRDEGCGAGDEKEQSHRPFLMLQAROSEDP 303
OY 231 HRYRRRGIDQGGSRMCCROEFFVDFREIGNNDWITIOPEGYAMNFCGOCPLHVAQMPGI 290
DB 304 HRRRRRGLECDGKVNICCKKOFVSPFKDIGNNDWITAPSGYHANYCEGECPSHIACTSGS 363
OY 291 SASFTAVLNLKANAAGTTGRGCCVPTSRRLSLLYDRDSNIVKTDIPDMVVEACG 350
DB 364 SLFSHTVINHYMRGHSPPFANLKSCCVPTKLRPMMLLYDDQNTIKKDIQNMIVEECG 423
OY 351 CS 352
DB 424 CS 425

```

Search completed: October 12, 2002, 02:09:56  
 Job time : 28 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

# OM protein - protein search, using sw model

Run on: October 11, 2002, 22:35:53 ; Search time 13.5 Seconds  
(without alignments)  
1009.576 Million cell updates/sec

Title: us-09-684-383-4

Perfect score: 1850  
Sequence: 1 MASSLLALLFLPTTVVNP.....DSNIVKTDIPDMVEACGCS 352

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1844	99.7	352	1	IHBC_MOUSE
2	1621.5	87.6	351	1	IHBC_RAT
3	1398	75.6	352	1	IHBC_HUMAN
4	594	32.1	350	1	IHBE_HUMAN
5	589.5	31.9	350	1	IHBE_RAT
6	581.5	31.4	350	1	IHBE_MOUSE
7	556	30.1	391	1	IHBC_CHICK
8	551	29.8	408	1	IHBB_BOVIN
9	548.5	29.6	407	1	IHBB_HUMAN
10	546	29.5	349	1	IHBB_PIG
11	543	29.4	424	1	IHBA_PIG
12	540	29.2	426	1	IHBA_HUMAN
13	538	29.1	424	1	IHBA_MOUSE
14	538	29.1	424	1	IHBA_RAT
15	534	28.9	426	1	IHBA_HORSE
16	532.5	28.8	425	1	IHBA_BOVIN
17	529.5	28.6	425	1	IHBA_SHEEP
18	494	26.7	424	1	IHBA_CHICK
19	456	24.6	255	1	IHBB_MOUSE
20	320	17.3	407	1	GDFF_HUMAN
21	316	17.1	405	1	GDFF_MOUSE
22	296	16.0	374	1	GDFF_BRARE
23	295	15.9	375	1	GDFF_SHEEP
24	290	15.7	375	1	GDFF_HUMAN
25	289	15.6	375	1	GDFF_MOUSE
26	288	15.6	375	1	GDFF_PAPIA
27	287	15.5	376	1	GDFF_PIG
28	287	15.5	376	1	GDFF_RAT
29	283	15.3	375	1	GDFF_BOVIN
30	283	15.3	375	1	GDFF_MELGA
31	282	15.2	375	1	GDFF_CHICK
32	273	14.8	365	1	BMP2_HUMAN
33	272	14.7	345	1	GDFF_RAT

34	263.5	14.2	395	1	BMP2_RABIT	046564 oryctolagus
35	261.5	14.1	393	1	BMP2_RAT	P49001 ratius norv
36	260.5	14.1	396	1	BMP2_DANDA	019006 dama dama (
37	257	13.9	394	1	BMP2_MOUSE	P21274 mus musculu
38	252.5	13.6	372	1	GDFF_HUMAN	P27539 homo sapien
39	252.5	13.6	401	1	BMP4_XENLA	P30885 xenopus lae
40	249	13.5	357	1	GDFF_MOUSE	P20863 mus musculu
41	248	13.4	454	1	BMP5_HUMAN	P22003 homo sapien
42	246	13.3	402	1	BMP8_HUMAN	P34820 homo sapien
43	244.5	13.2	353	1	BMP2_CHICK	090751 gallus galli
44	244.5	13.2	510	1	BMP6_MOUSE	P20722 mus musculu
45	243.5	13.2	408	1	BMP4_DANDA	029607 dama dama (

## ALIGNMENTS

RESULT 1  
ID IHBC\_MOUSE STANDARD: PRT: 352 AA.  
AC P5104: Q61452;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inhibin beta C chain precursor (Activin beta-C chain).  
GN INHBC.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=129; TISSUE=Liver;  
RX MEDLINE=96435913; PubMed=8838799;  
RA Schmitt J., Hoelten G., Jenkins N.A., Gilbert D.J., Copeland N.G.,  
RA Pohl J., Schrewe H.;  
RT "Structure, chromosomal localization, and expression analysis of the  
RT mouse inhibin/activin beta C (inhbc) gene.";  
RL Genomics 32:358-366(1996).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96283807; PubMed=8679697;  
RA Lau A.L., Nishimori K., Matzuk M.M.;  
RT "Structural analysis of the mouse activin beta C gene.";  
RL Biochim. Biophys. Acta 1307:145-148(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97224404; PubMed=9070865;  
RA Fang J., Wang S.Q., Smiley E., Bonadio J.;  
RT "Genes coding for mouse activin beta C and beta E are closely linked  
RT and exhibit a liver-specific expression pattern in adult tissues.";  
RL Biochem. Biophys. Res. Commun. 231:655-661(1997).  
RN [4]  
RP FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
CC ACTIVINS.  
CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
CC SIMILARITY).  
CC -1- TISSUE SPECIFICITY: MAINLY EXPRESSED IN THE ADULT LIVER.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
CC  
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CC EMBL: X90841; CAA62347.1; -  
 CC EMBL: X90842; CAA62347.1; JOINED.  
 CC EMBL: X90819; CAA62333.1; -  
 CC EMBL: U40773; AAC52723.1; -  
 CC EMBL: U40772; AAC52723.1; JOINED.  
 CC EMBL: U95962; AAC53164.1; -  
 CC HSSP: P18075; IBMP.  
 CC MGD: MGI:105932; InhbC.  
 CC InterPro: IPR002400; GF\_CysKnot.  
 CC InterPro: IPR001318; Inhibin\_betaC.  
 CC InterPro: IPR001839; TGF-beta.  
 CC Pfam: PF00019; TGF-beta; 1.  
 CC PRINTS: PR00438; GECYSKNOT.  
 CC PRINTS: PR00672; INHIBINB.  
 CC PRODOM: PD000357; TGF-beta; 1.  
 CC SMART: SM00204; TGF-beta; 1.  
 CC PROSITE: PS00250; TGF\_BETA\_1; 1.  
 CC Growth factor: Hormone: Glycoprotein: Signal.  
 CC SIGNAL: 18  
 CC PROPEP: 19 236  
 CC CHAIN: 237 352  
 CC DISULFID: 240 248  
 CC DISULFID: 247 317  
 CC DISULFID: 276 349  
 CC DISULFID: 280 351  
 CC DISULFID: 316 316  
 CC CARBOHYD: 113 111  
 CC CARBOHYD: 143 143  
 CC CARBOHYD: 151 151  
 CC CARBOHYD: 173 173  
 CC CONFLICT: 243 243  
 CC SEQUENCE: 352 AA; 39401 MW; 220812FD73717185 CRC64;

Query Match 99.7%; Score 1844; DB 1; Length 352;  
 Best Local Similarity 99.7%; Pred. No. 4.8e-164;  
 Matches 351; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MASSLLALLFLPTTVVNPKEGPCACGATDLSORELLDLAKSILDKLHLSOR 60  
 DB 1 MASSLLALLFLPTTVVNPKEGPCACGATDLSORELLDLAKSILDKLHLSOR 60  
 OY 61 PILSRPVSGALKTALORLGRPRRETLLEHDOQREYEELISFADTDLSSINOTRLEPHFS 120  
 DB 61 PILSRPVSGALKTALORLGRPRRETLLEHDOQREYEELISFADTDLSSINOTRLEPHFS 120  
 OY 121 GMAAGMEVYRQTRFMFVOPHNATOTMIRVLRLPYDTNLTLSQYVVOVNASGWYQL 180  
 DB 121 GMAAGMEVYRQTRFMFVOPHNATOTMIRVLRLPYDTNLTLSQYVVOVNASGWYQL 180  
 OY 181 LIGPNAQAAGSGHLLLELVPEQVAHSSILTGWFSHRPVAAGVREKRRRRGIDC 240  
 DB 181 LIGPNAQAAGSGHLLLELVPEQVAHSSILTGWFSHRPVAAGVREKRRRRGIDC 240  
 OY 241 OGASNMCRHOFVDFRELGMDNMIIOPEGYANNECTGOCPLHYAGMGISASPTAVLN 300  
 DB 241 OGASNMCRHOFVDFRELGMDNMIIOPEGYANNECTGOCPLHYAGMGISASPTAVLN 300  
 OY 301 LKANAAGATTGRCSCCVTSRRPLSLLYYDRDSNIYKTDIPDWVVEAGCS 352  
 DB 301 LKANAAGATTGRCSCCVTSRRPLSLLYYDRDSNIYKTDIPDWVVEAGCS 352

RESULT 2  
 ID INHC\_RAT STANDARD: PRT: 351 AA.  
 AC OG9WUK5;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Inhibin beta C chain precursor (Activin beta-C chain).  
 GN INHC.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 CC NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar;  
 RA Rossmann W., Peter B., Schulte-Hermann R.;  
 RT "Rat activin beta C and beta E: sequence and expression";  
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
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DR EMBL: AF140031; AAD30132.1; -  
 DR HSSP: P18075; IBMP.  
 DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR001318; Inhibin\_betaC.  
 DR InterPro: IPR001839; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIBINA.  
 DR PRINTS: PR00672; INHIBINB.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor: Hormone: Glycoprotein: Signal.  
 DR SIGNAL: 18  
 DR PROPEP: 19 236  
 DR CHAIN: 237 351  
 DR DISULFID: 239 246  
 DR DISULFID: 246 316  
 DR DISULFID: 275 348  
 DR DISULFID: 279 350  
 DR DISULFID: 315 315  
 DR CARBOHYD: 110 110  
 DR CARBOHYD: 142 142  
 DR CARBOHYD: 160 160  
 DR SEQUENCE: 351 AA; 39335 MW; 6B219BF6C3E180A1 CRC64;

Query Match 87.6%; Score 1621.5; DB 1; Length 351;  
 Best Local Similarity 89.5%; Pred. No. 2.4e-143;  
 Matches 315; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

OY 1 MASSLLALLFLPTTVVNPKEGPCACGATDLSORELLDLAKSILDKLHLSOR 60  
 DB 1 MASSLLALLFLPTTVVNPKEGPCACGATDLSORELLDLAKSILDKLHLSOR 60  
 OY 61 PILSRPVSGALKTALORLGRPRRETLLEHDOQREYEELISFADTDLSSINOTRLEPHFS 120  
 DB 61 PILSRPVSGALKTALORLGRPRRETLLEHDOQREYEELISFADTDLSSINOTRLEPHFS 119

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OY 121 GRMAGMEVROTRFMEFVOPPHNATOTMNIHVLYLPYDTNLTLSQVYVYVNASGMWYQ 180
DB 120 DRTGCGVEVLOTREMFQOLRPNTTQMINIRVLYRPYDTNLTLSQVLYQVADASGMWYQ 179
OY 181 LLGPEAQAACSGHUTLTELVEPESQVASHLLGFWFRRPFAVAQVRECKHVRRGIDC 240
DB 180 LLGPEAQAACSGHUTLTELVEPESQVASHLLGFWFRRPFAVAQVRECKHVRRGIDC 239
OY 241 CGGSRMCCROEFFVDFREIGMNDWITIOPEGYAMNCTGCPPLHAGMPCISASFHTAVLN 300
DB 240 CGGSRMCCROEFFVDFREIGMNDWITIOPEGYAMNCTGCPPLHAGMPCISASFHTAVLN 299
OY 301 LLKNNAAAGTGRGSCCVPTRSRPLSLLYDRDSNVKTDIDPMVEACGCS 352
DB 300 LLKNNAAAGTGRGSCCVPTRSRPLSLLYDRDSNVKTDIDPMVEACGCS 351

RESULT 3
ID IHBC_HUMAN STANDARD: PRT: 352 AA.
AC P5103;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inhibin beta C chain precursor (Activin beta-C chain).
GN INHBC.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
ON (1)
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RX MEDLINE=95126951; PubMed=7826378;
RA Hostetter C., Neidhardt H., Schneider C., Pohl J.;
RT "Cloning of a new member of the TGF-beta family: a putative new
RL Blochman. Biophys. Res. Commun. 206:608-613(1995).
RN (2)
RP TISSUE SPECIFICITY.
RX MEDLINE=96089987; PubMed=9428386;
RA Thomas T.Z., Chapman S.M., Hong W., Gursingfhe C., Mellor S.L.,
RA Fletcher R., Pedersen J., Rishbidge G.P.;
RT "Inhibins, activins, and follistatins: expression of mRNAs and
RT cellular localization in tissues from men with benign prostatic
hyperplasia.";
RL Prostate 34:34-43(1998).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDENT ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.
CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
CC SIMILARITY).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN BENIGN PROSTATIC HYPERPLASIA.
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
CC -----
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: X82540; CAA57890.1; -

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DR HSSP: P18075; 1BMP.
DR MIM: 601233; -.
DR InterPro: IPR002400; GF_cysknot.
DR InterPro: IPR001318; Inhibin_betaC.
DR InterPro: IPR001839; TGF-beta.
DR Pfam: PF00019; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00672; INHIBINBC.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGF-beta; 1.
DR PROSITE: PS00250; TGF-BETA_1; 1.
DR Growth factor; Hormone; Glycoprotein; Signal.
KM STGNAL 1 18
FT PROPEP 19 236
FT CHAIN 237 352
FT DISULFID 240 248
FT DISULFID 247 317
FT DISULFID 276 349
FT DISULFID 280 351
FT DISULFID 316 316
FT CARBOHYD 110 110
FT CARBOHYD 143 143
FT CARBOHYD 161 161
SQ SEQUENCE 352 AA; 38238 MW; 496476AD82562D3E CRC64;

Query Match 75.6%; Score 1398; DB 1; Length 352;
Best Local Similarity 76.2%; Pred. No. 1.5e-122;
Matches 269; Conservative 32; Mismatches 50; Indels 2; Gaps 2;

OY 1 MASSLLALLPLPTTYVNPKEGCPACMGALFQLESORELLDLAKSLDKLILSOR 60
DB 1 MTSSLLAFLLAPPTVTPRAGGCPACGPTLESORELLDLAKSLDKLILTOR 60
OY 61 PILSRVSRGALKTALQRLPRRETLLEHDOREYELISFADTLSSINOTRELFHFS 120
DB 61 PTLNRPVRAALRTALQHLHGVQCALF-DKREDCEILSFREGLSTINOTRDLPHFS 119
OY 121 G-RMAGMEVROTRFMEFVOPPHNATOTMNIHVLYLPYDTNLTLSQVYVYVNASGMWYQ 179
DB 120 SDRTAGDREYQASLMEFQOLRPNTTQMINIRVLYLPYDTNLTLSQVLYQVADASGMWYQ 179
OY 180 LLGPEAQAACSGHUTLTELVEPESQVASHLLGFWFRRPFAVAQVRECKHVRRGID 239
DB 180 LLGPEAQAACSGHUTLTELVEPESQVASHLLGFWFRRPFAVAQVRECKHVRRGID 239
OY 240 CGGSRMCCROEFFVDFREIGMNDWITIOPEGYAMNCTGCPPLHAGMPCISASFHTAVLN 299
DB 240 CGGSRMCCROEFFVDFREIGMNDWITIOPEGYAMNCTGCPPLHAGMPCISASFHTAVLN 299
OY 300 LLKNNAAAGTGRGSCCVPTRSRPLSLLYDRDSNVKTDIDPMVEACGCS 352
DB 300 LLKNNAAAGTGRGSCCVPTRSRPLSLLYDRDSNVKTDIDPMVEACGCS 352

RESULT 4
ID IHBC_HUMAN STANDARD: PRT: 350 AA.
AC P58166;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta E chain precursor (Activin beta-E chain).
GN INHBE.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OC NCBI_TaxID=9606;
ON (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Rhabdomyosarcoma;
RA Strausberg R.;
RT Submitted (MAR-2001) to the EMBL/Genbank/DDA databases.
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,

```

CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: BC005161; AAH05161.1;  
 CC Interpro: IPR002405; Inhibin\_alpha.  
 CC Interpro: IPR001318; Inhibin\_betaC.  
 CC Interpro: IPR001839; TGF-beta.  
 CC Pfam: PF00019; TGF-beta; 1.  
 CC PRINTS: PR00669; INHIBIN.  
 CC PRINTS: PR00672; INHIBIN.  
 CC Prodom: PD000357; TGF-beta; 1.  
 CC SMART: SM00204; TGF-beta; 1.  
 CC PROSITE: PS00250; TGF-BETA\_1; 1.  
 CC Growth factor: Hormone; Glycoprotein; signal.  
 CC FT SIGNAL 1 19 POTENTIAL.  
 CC FT PROPEP 20 236 POTENTIAL.  
 CC FT CHAIN 237 350 INHIBIN BETA E CHAIN.  
 CC FT DISULFID 240 248 BY SIMILARITY.  
 CC FT DISULFID 247 315 BY SIMILARITY.  
 CC FT DISULFID 276 347 BY SIMILARITY.  
 CC FT DISULFID 280 349 BY SIMILARITY.  
 CC FT DISULFID 314 314 BY SIMILARITY.  
 CC FT CARBOHYD 198 198 INTERCHAIN (BY SIMILARITY).  
 CC SEQUENCE 350 AA; 38561 MW; A49C1495677E3EEF CMC64; (POTENTIAL).

Query Match 32.1%; Score 594; DB 1; Length 350;  
 Best Local Similarity 39.38; Pred. No. 9.3e-46;  
 Matches 141; Conservative 51; Mismatches 109; Indels 58; Gaps 11;

CC 22 TEGPCPACGAIPLDESORELLDLAKSLDKLHLSORPLSRPVSRGALKTALQRLR- 80  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 22 TGVGVPSCGSKLAPQERLVLELAKQQLDGLHLSRPRITPPRALALTRALRRDLP 81  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 81 ---GRRRETLLEHDOKEEYIISPAD-TDLSSINQRLFEHFGSRMAGSEVROTRWF-136  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 82 GSAVAGNGE-----EVISFAVTDTSTAYSSSLTFHLS--PRSHNLVYARLML 128  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 137 FVGFHNMATOTMNI-----RVLYLRPDNTLTLTLYQVVOVNASGWQLLGP 184  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 129 HVLPLPLGTLCLRIEFGMRGRRRRRQSGRTLLAEHHTNL-----GMHTLTLPS 175  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 185 EAOACSGCHLTLELVPEBOVAHSSL-----ILGWFSH-RPFVAQVRYE--GKHRRR 235  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 176 SGLREKSVLQLDLCDRLLEGSTVYGOPRRLLDTAGHOPPLLEKLRANPEGARRR 235  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 236 RIGIDCGSRMCCRFYVDFEIGNNDMTIQEGYAMNFCGCPHVAQPGTSASFH @95  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 236 RTPTCEPATPLICCRKHRYVDFOLGKRWMLQPEGVOLNCSGCCPHLASSPGIAASFH 295  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 296 TAVLNLKANA--AAGTGRSGCCVPTSRRLSLLYYDRDSNIYKTDIPDVVEACGS 352  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC 296 SAVFSLKANNMPAST-----SCCVPTARRPLSLLYLDHNGVYKTDVPMVVEACGS 350  
 CC | | | | | : : : : : | | | | | : : : : : | | | | | : : : : :  
 CC Db

RESULT 5  
 ID HIBE\_RAT STANDARD: PRT: 350 AA.  
 AC 08859; Q9R285;  
 DT 15-JUL-1999 (Rel. 38, Created)  
 DT 15-JUL-1999 (Rel. 38, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta E chain precursor (Activin beta-E chain).  
 GN INHE.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OC NCBI\_TaxID=10116;  
 RP [1]  
 RC SEQUENCE FROM N.A.  
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=Liver, and Lung;  
 RX MEDLINE=20290891; PubMed=10828834;  
 RA O'Bryan M.K., Sebire K.L., Gerdsraert O., Hedger M.P., Hearn M.T.W.,  
 RA de Kretser D.M.;  
 RT "Cloning and regulation of the rat activin beta subunit."  
 RL J. Mol. Endocrinol. 24:409-418(2000).  
 [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Wistar;  
 RA Rossmann W., Peter H., Schulte-Hermann R.;  
 RT "Rat activin beta C and beta E: sequence and expression."  
 RL Submitted (Apr-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC AXIAL DEVELOPMENT, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH  
 CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.  
 CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY  
 CC SIMILARITY).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF089825; AAC36741.1;  
 CC EMBL: AF140032; AAD30133.1;  
 CC HSSP: P12643; 38MP.  
 CC Interpro: IPR002400; GF\_cysknot.  
 CC Interpro: IPR001318; Inhibin\_betaC.  
 CC Interpro: IPR001839; TGF-beta.  
 CC Pfam: PF00019; TGF-beta; 1.  
 CC PRINTS: PR00438; GFCYSKNOT.  
 CC PRINTS: PR00672; INHIBIN.  
 CC Prodom: PD000357; TGF-beta; 1.  
 CC SMART: SM00204; TGF-beta; 1.  
 CC PROSITE: PS00250; TGF-BETA\_1; 1.  
 CC Growth factor: Hormone; Glycoprotein; signal.  
 CC FT SIGNAL 1 21 POTENTIAL.  
 CC FT PROPEP 22 236 POTENTIAL.  
 CC FT CHAIN 237 350 INHIBIN BETA E CHAIN.  
 CC FT DISULFID 240 248 BY SIMILARITY.  
 CC FT DISULFID 247 315 BY SIMILARITY.  
 CC FT DISULFID 276 347 BY SIMILARITY.  
 CC FT DISULFID 280 349 BY SIMILARITY.  
 CC FT DISULFID 314 314 BY SIMILARITY.  
 CC INTERCHAIN (BY SIMILARITY).

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FT CAROHYD 198 198 N-Linked (GLCNAC... ) (POTENTIAL).
FT CONFLICT 160 161 EH -> DY (IN REF. 2).
SO SEQUENCE 350 AA; 38898 MW; 0CBFF6E10E926E3 CRC64;

Query Match 31.9%; Score 589.5; DB 1; Length 350;
Best Local Similarity 39.2%; Pred. No. 2, 4e-47;
Matches 144; Conservative 54; Mismatches 122; Indels 47; Gaps 12.

OY 5 LLLALLFLPTTVVNPKEGPCPCACGATFDLESQRELLDLAKSILDKLHLSQRPILS 64
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 12 LLMALAMV-----QSTRSACPSGCAPIITPGCEGRALVLELAKQOILEGLHLSRPRIT 64
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
OY 65 RPRSRGALKALALALRGR-----RETLLEHQROREFEYIISFADPLSSINOTRLEFH 118
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 65 RPLPQALFLTRALRLQ--PRSNVPGNRE-----KVISFATSIDKSTSTVRSYLT 111
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
OY 119 FSGRMASGMEVROGRPFMEVQPRFNATQMTNIRVLRLRPDNTLILSQVYVQVNASGMX 178
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 112 FQLSPLMSHHLVHARLWLHV--PRSPRALYLTIFECGTTTRCRGSRFLAEHQTTSSGMH 169
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
OY 179 QULLLPEAOAASOG--HLTLELV---ESQVASSLLT-----GWFSPRPVAAQVRE- 228
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 170 ALTLPSGLARSEEGVTKQLQLEFRRLDLNSTARLRRLRLDLDTAG--QQRPLELKRANE 227
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
OY 229 -GKHRYVRRGIDCGGSRMCCRQEPFVDFREIGMNDMIIOPEGYAMNFCTGCPLHVGM 287
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 228 PGAGRRARRRPTCTSEPRFLCCGRDHYVDQELQRMIIQPEGQLNYCSQCCPHLAGS 287
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
OY 288 PGISASFHTAVLNLIKANA--AAGTTGSGCCVPTSRRLSLLYDRDSNIKTDIPDMV 345
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 288 PGIAASHSYAVSILKANNPWPAGS---SCGVPTARRPLSLYLIDHNGVNVKTDVPMV 343
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
OY 346 VEACGCS 352
   |||::: |||::: |||::: |||::: |||::: |||::: |||::: |||:::
DB 344 VEACGCS 350

RESULT 6
THBE_MOUSE STANDARD: PRT: 350 AA.
1HBE_MOUSE
1D THBE_MOUSE
AC 008717;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta E chain precursor (Activin beta-E chain).
GN THBE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus.
OC NCBI_TaxID=10090;
OY 11
RN RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA MEDLINE=97096313; PubMed=8941337;
RA Fang J., Yin W., Smiley E., Wang S.O., Bonadio J.;
RT "Molecular cloning of the mouse activin beta E subunit gene.";
RL Biochem. Biophys. Res. Commun. 228:665-674(1996).
RN 12
RP SEQUENCE FROM N.A.
RP MEDLINE=97224404; PubMed=9070865;
RA Fang J., Wang S.O., Smiley E., Bonadio J.;
RT "Genes coding for mouse activin beta C and beta E are closely linked
and exhibit a liver-specific expression pattern in adult tissues.";
RL Biochem. Biophys. Res. Commun. 231:655-661(1997).
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.
CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
CC FUNCTIONS SUCH AS HYPOTHALMIC AND PITUITARY HORMONE SECRETION,
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
CC ACTIVINS.

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CC -1 SUBUNIT: HOMODIMERIC OR HETERODIMERIC THROUGH ASSOCIATION WITH
CC ALPHA AND BETA SUBUNITS, LINKED BY ONE OR MORE DISULFIDE BONDS.
CC INHIBINS ARE HETERODIMERS OF ONE ALPHA AND ONE BETA SUBUNIT.
CC ACTIVINS ARE HOMO-OR HETERODIMERS OF BETA SUBUNITS ONLY (BY
CC SIMILARITY).
CC -1 DEVELOPMENTAL STAGE: FIRST EXPRESSION IN EMBRYONIC LIVER IS
CC DETECTED AT DAY E17.5.
CC -1 SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
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-----
CC DR EMBL; U96386; AAB53801.1; -.
CC DR HSSP; P12643; 3BMP.
CC DR MGI; MGI:109269; Inhbe.
CC DR InterPro; IPR002400; GF_cysknot.
CC DR InterPro; IPR001318; InhIdin_betaC.
CC DR InterPro; IPR001839; TGF-beta.
CC DR Pfam; PF00019; TGF-beta; 1.
CC DR PRINTS; PR00438; GFCYSKNOT.
CC DR PRINTS; PR00672; INHIBINBC.
CC DR ProDom; PD000357; TGF-beta; 1.
CC DR SMART; SM00204; TGFb; 1.
CC DR PROSITE; PS00250; TGF_BETA_1; 1.
CC KM Growth factor; Hormone; Glycoprotein; Signal.
CC FT SIGNAL; 1 21 POTENTIAL.
CC FT PROPEP; 22 236 POTENTIAL.
CC FT CHAIN; 237 350 INHIBIN BETA E CHAIN.
CC FT DISULFID; 240 248 BY SIMILARITY.
CC FT DISULFID; 247 315 BY SIMILARITY.
CC FT DISULFID; 276 347 BY SIMILARITY.
CC FT DISULFID; 280 349 BY SIMILARITY.
CC FT DISULFID; 314 314 INTERCHAIN (BY SIMILARITY).
CC FT CARBOHYD; 198 198 N-LINKED (GLCNAC... ) (POTENTIAL).
CC SQ SEQUENCE 350 AA; 39057 MW; F37C76C8061D8AD9 CRC64;

Query Match 31.4%; Score 581.5; DB 1; Length 350;
Best Local Similarity 37.7%; Pred. No. 1.4e-46;
Matches 140; Conservative 66; Mismatches 110; Indels 55; Gaps 14;

QY 5 LLLALLFLEPTTVVNPKTGCPACGALFDESORELLDLDAKKSILDKLHLSORPLLS 64
DB 12 LLMALVAV-----QSRNSACPSGCGPRLPAOGERALVLELAKQQLLEGHLNLSRPIT 64
QY 65 RPYVSRGALKTALORLRCGR-----RETLLEHDQROEEYEIISFAD--TDLSSINOTRLE 116
DB 65 RPLPQALTRALRLRQ--PKSNVPGNRE-----KVISPATIIDKSTSYRSMULT 111
QY 117 FHSGRMASGHEVQOTRMFFVQOPHNATOTMINIRVLYLRPYDTNL-----TLTSQYVYVQ 172
DB 112 FOLSPLTSMHNL-----YHARLMLHVPPSPFQTYLIR--IFRCGTTTRGRGFLEAH--QT 163
QY 173 NASGWYOLLCPREAOACSOGLHTELE-----VPSQVANHSSILLGWF--SHRPVAAOV 225
DB 164 TSSGWMALTLTPSSGURSDSGVVKQLDERPLDLNMTAGLPRLDLDTAGQOARPLELKI 223
QY 226 RVE--GCHRVRRRGIDQGGSNMCRQEFVVFRELGMNDWIIIOPEGYANMFQGGCPHL 283
DB 224 RANEPGCGRRARRRPTCPPEPLPLCCRRDHYVFOELGMKRWMLLLOPEGYOLVYCGGQCPH 283
QY 284 VACMPGASAPHTAVLNLTAKANA--AAGTGTGSGCCVPTSRRLPSLLYYDRDSINVKTDI 341
DB 284 LAQSPGTAASFHSAVFSLKANNPWAGS-----SCCVPTARRPLSLLYLDHNGVAKTDV 339
QY 342 PDMVVEAGCS 352
DB 340 PDMVVEAGCS 350

```

RESULT 7  
ID HBb\_CHICK STANDARD: PRT: 391 AA.  
AC HBb\_CHICK P27093: 073796;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Inhibin beta B chain precursor (Activin beta-B chain).  
GN HBb.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OC NCBL\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Pollicle;  
RA Klingner H., Hatacschek-Wiener J., Mohirab B.K., Kuchler K., Mohirab F.;  
RL submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=WHITE LEGHORN; TISSUE=Ovary;  
RA Hecht D.J., Davis A.J., Ryan I.M., Johnson P.A.;  
RL submitted (MAR-1998) to the EMBL/Genbank/DBJ databases.  
RN [3]  
RP SEQUENCE OF 311-381 FROM N.A.  
RX MEDLINE=91029482; PubMed=2225063;  
RA Mitsani E., Ziv T., Thomsen G., Shitmoni Y., Melton D.A., Brill A.;  
RT Activin can induce the formation of axial structures and is expressed  
RL in the hypoblast of the chick.";  
Cell 63:495-501(1990).  
CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
CC RESECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
CC ACTIVINS.  
CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
-----  
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CC EMBL: Z71594; CAA96248.1; -  
CC EMBL: AF055478; AAC14187.1; -  
CC EMBL: M61166; AAA48568.1; -  
CC EMBL: M57408; AAA03079.1; -  
CC HSSP: P18075; IBMP.  
CC InterPro: IPR002400; GF\_cysknot.  
CC InterPro: IPR001839; TGF\_beta.  
CC InterPro: IPR001111; TGFb\_N.  
CC Pfam: PF00019; TGF-beta; 1.  
CC Pfam: PF00688; TGF-beta; 1.  
CC PRINTS: PR00438; GRCYSKNO.  
CC ProDom: PD000357; TGF-beta; 1.  
CC SMART: SM00204; TGFb; 1.  
CC PROSITE: PS00250; TGF\_BETA1; 1.  
CC Growth factor: Hormone; Glycoprotein; Signal.  
CC SIGNAL: 1 25 POTENTIAL.

Query Match	Best Local Similarity	Matches	Score	DB 1;	Length	DB 2;	Score	DB 3;	Length	DB 4;	Score	DB 5;	Length	DB 6;	Score	DB 7;	Length	DB 8;	Length	DB 9;	Score	DB 10;	Length	DB 11;	Score	DB 12;	Length	DB 13;	Score	DB 14;	Length	DB 15;	Score	DB 16;	Length	DB 17;	Score	DB 18;	Length	DB 19;	Score	DB 20;	Length	DB 21;	Score	DB 22;	Length	DB 23;	Score	DB 24;	Length	DB 25;	Score	DB 26;	Length	DB 27;	Score	DB 28;	Length	DB 29;	Score	DB 30;	Length	DB 31;	Score	DB 32;	Length	DB 33;	Score	DB 34;	Length	DB 35;	Score	DB 36;	Length	DB 37;	Score	DB 38;	Length	DB 39;	Score	DB 40;	Length	DB 41;	Score	DB 42;	Length	DB 43;	Score	DB 44;	Length	DB 45;	Score	DB 46;	Length	DB 47;	Score	DB 48;	Length	DB 49;	Score	DB 50;	Length	DB 51;	Score	DB 52;	Length	DB 53;	Score	DB 54;	Length	DB 55;	Score	DB 56;	Length	DB 57;	Score	DB 58;	Length	DB 59;	Score	DB 60;	Length	DB 61;	Score	DB 62;	Length	DB 63;	Score	DB 64;	Length	DB 65;	Score	DB 66;	Length	DB 67;	Score	DB 68;	Length	DB 69;	Score	DB 70;	Length	DB 71;	Score	DB 72;	Length	DB 73;	Score	DB 74;	Length	DB 75;	Score	DB 76;	Length	DB 77;	Score	DB 78;	Length	DB 79;	Score	DB 80;	Length	DB 81;	Score	DB 82;	Length	DB 83;	Score	DB 84;	Length	DB 85;	Score	DB 86;	Length	DB 87;	Score	DB 88;	Length	DB 89;	Score	DB 90;	Length	DB 91;	Score	DB 92;	Length	DB 93;	Score	DB 94;	Length	DB 95;	Score	DB 96;	Length	DB 97;	Score	DB 98;	Length	DB 99;	Score	DB 100;	Length	DB 101;	Score	DB 102;	Length	DB 103;	Score	DB 104;	Length	DB 105;	Score	DB 106;	Length	DB 107;	Score	DB 108;	Length	DB 109;	Score	DB 110;	Length	DB 111;	Score	DB 112;	Length	DB 113;	Score	DB 114;	Length	DB 115;	Score	DB 116;	Length	DB 117;	Score	DB 118;	Length	DB 119;	Score	DB 120;	Length	DB 121;	Score	DB 122;	Length	DB 123;	Score	DB 124;	Length	DB 125;	Score	DB 126;	Length	DB 127;	Score	DB 128;	Length	DB 129;	Score	DB 130;	Length	DB 131;	Score	DB 132;	Length	DB 133;	Score	DB 134;	Length	DB 135;	Score	DB 136;	Length	DB 137;	Score	DB 138;	Length	DB 139;	Score	DB 140;	Length	DB 141;	Score	DB 142;	Length	DB 143;	Score	DB 144;	Length	DB 145;	Score	DB 146;	Length	DB 147;	Score	DB 148;	Length	DB 149;	Score	DB 150;	Length	DB 151;	Score	DB 152;	Length	DB 153;	Score	DB 154;	Length	DB 155;	Score	DB 156;	Length	DB 157;	Score	DB 158;	Length	DB 159;	Score	DB 160;	Length	DB 161;	Score	DB 162;	Length	DB 163;	Score	DB 164;	Length	DB 165;	Score	DB 166;	Length	DB 167;	Score	DB 168;	Length	DB 169;	Score	DB 170;	Length	DB 171;	Score	DB 172;	Length	DB 173;	Score	DB 174;	Length	DB 175;	Score	DB 176;	Length	DB 177;	Score	DB 178;	Length	DB 179;	Score	DB 180;	Length	DB 181;	Score	DB 182;	Length	DB 183;	Score	DB 184;	Length	DB 185;	Score	DB 186;	Length	DB 187;	Score	DB 188;	Length	DB 189;	Score	DB 190;	Length	DB 191;	Score	DB 192;	Length	DB 193;	Score	DB 194;	Length	DB 195;	Score	DB 196;	Length	DB 197;	Score	DB 198;	Length	DB 199;	Score	DB 200;	Length	DB 201;	Score	DB 202;	Length	DB 203;	Score	DB 204;	Length	DB 205;	Score	DB 206;	Length	DB 207;	Score	DB 208;	Length	DB 209;	Score	DB 210;	Length	DB 211;	Score	DB 212;	Length	DB 213;	Score	DB 214;	Length	DB 215;	Score	DB 216;	Length	DB 217;	Score	DB 218;	Length	DB 219;	Score	DB 220;	Length	DB 221;	Score	DB 222;	Length	DB 223;	Score	DB 224;	Length	DB 225;	Score	DB 226;	Length	DB 227;	Score	DB 228;	Length	DB 229;	Score	DB 230;	Length	DB 231;	Score	DB 232;	Length	DB 233;	Score	DB 234;	Length	DB 235;	Score	DB 236;	Length	DB 237;	Score	DB 238;	Length	DB 239;	Score	DB 240;	Length	DB 241;	Score	DB 242;	Length	DB 243;	Score	DB 244;	Length	DB 245;	Score	DB 246;	Length	DB 247;	Score	DB 248;	Length	DB 249;	Score	DB 250;	Length	DB 251;	Score	DB 252;	Length	DB 253;	Score	DB 254;	Length	DB 255;	Score	DB 256;	Length	DB 257;	Score	DB 258;	Length	DB 259;	Score	DB 260;	Length	DB
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DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF000688; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR PRINTS: PRO00438; GFCISNOT.  
 DR PRINTS: PRO00671; INHIBINB.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-beta; 1.  
 KW Growth factor; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1 28  
 FT PROPEP 29 232  
 FT CHAIN 29 232  
 FT DISULFID 293 407  
 FT DISULFID 296 304  
 FT DISULFID 303 372  
 FT DISULFID 332 404  
 FT DISULFID 336 406  
 FT DISULFID 371 371  
 FT CARBOHYD 93 93  
 FT CONFLICT 47 47  
 FT SEQUENCE 407 AA; 45121 MW; 90316C83597BA64 CRC64;  
 Query Match 29.6%; Score 548.5; DB 1; Length 407;  
 Best Local Similarity 33.3%; Pred. No. 1.9e-43;  
 Matches 134; Conservative 66; Mismatches 145; Indels 57; Gaps 13:  
 QY 2 ASSLLALLFL-----TPTVVNPKEGP-----CPACWGAIFDLESOREL 42  
 DB 12 ACLLLAAGMLPEAMGSPPTPPAPPPPPGSGSDTCTSCG-----FRRPEL 67  
 QY 43 -----LIDLAKSILDKLHLSORPLISRPYSKALATLQRLR-GPRRE---TLLEH-- 90  
 DB 68 GRVDDDFEAVNRHILSRLOMRPRNTHAVPKAMVTALEKLHAGKVRDEGRVEIPIHD 127  
 QY 91 -----DQROEEYEIISFADTLLSSINOTRLEFHFSGRMASGMEVROTFRMFVVO-FPH 142  
 DB 128 CHASPGADGQERSEIISFADTLLSSINOTRLEFHFSGRMASGMEVROTFRMFVVO-FPH 187  
 QY 143 ---NATQTMNIRLVLPYDTNLTLSQYVVOVNASGYOLLGPEAQAACSGHLTLE 198  
 DB 188 VLEKGSRRKRVKVVYPOEGHGRMNMVKEKRVDLKRSQWHTFPLEALQALEKREKRLN 247  
 QY 199 LVPESQVAAHSLILGW-----SHRPFVAOAQV-BGKHVRVRRGIDCGGSRMCCROE 251  
 DB 248 LDVQDSCQELAVPVFVPGESHRPFVVOQARLGDSTRIRKRGLECDRTNLCRCQO 307  
 QY 252 FFVDREIGMNMIIIDPEGYAMNECTGCGPLHVAAGCIGASFTFVNLKANNA-AGT 310  
 DB 308 FFIDRLIGMNMIIIAFTGYGVNVCESCPAYLAGVPCSSSFTTAVVNOYRMRLNPGT 367  
 QY 311 TGRGSCCVPTSRRLPLSLYYRDSNIIVKTDIPDMVVEACGS 352  
 DB 368 V--NSCCIPTKLSTMSMLTFDEYNIVKRDVPMNIVECGCA 407  
 RESULT 10  
 ID IHHB\_PIG STANDARD; PRT: 349 AA.  
 AC P04088;  
 DT 01-NOV-1986 (Rel. 03, Created)  
 DT 01-NOV-1986 (Rel. 03, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta B chain precursor (Activin beta-B chain) (Fragment).  
 GN IHHB.  
 OS Sus scrofa (pig).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
 OX NCBI\_TaxID=9823;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovarian follicular fluid;  
 RX MEDLINE=66092207; PubMed=2417121;  
 RA "Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,

RA Guillemin R., Niall H., Seeburg P.H.;  
 RT "Complementary DNA sequences of ovarian follicular fluid inhibin show  
 RT precursor structure and homology with transforming growth  
 RT factor-beta.";  
 RL Nature 318:659-663(1985).  
 RN (2)  
 RP SEQUENCE OF 235-249.  
 RX MEDLINE=92355604; PubMed=1644823;  
 RA Nakamura T., Asashima M., Eto Y., Takio K., Uchiyama H., Moriya N.,  
 RA Aizumi T., Yashiro T., Sugino K., Tiltani K., Sugino H.;  
 RT "Isolation and characterization of native activin B.";  
 RL J. Biol. Chem. 267:16385-16389(1992).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: X03267; CAA27021.1;  
 CC DR PIR: A01394; WPGGB.  
 CC DR HSSP: P18075; IBMP.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-beta; 1.  
 KW Growth factor; Hormone; Glycoprotein.  
 FT NON\_TER 1 1  
 FT PROPEP <1 234  
 FT CHAIN 235 349  
 FT DISULFID 238 246  
 FT DISULFID 245 314  
 FT DISULFID 274 346  
 FT DISULFID 278 348  
 FT DISULFID 313 313  
 FT CARBOHYD 35 35  
 FT SEQUENCE 349 AA; 39354 MW; C571EN91ADASDE77 CRC64;  
 Query Match 29.5%; Score 546; DB 1; Length 349;  
 Best Local Similarity 35.8%; Pred. No. 2.7e-43;  
 Matches 120; Conservative 65; Mismatches 122; Indels 28; Gaps 9:  
 QY 44 IDLAKSILDKLHLSORPLISRPYSKALATLQRLR-GPRRE---TLLEH----- 90  
 DB 17 LEAVKRILNLRQKRGRRNTHAVPKAMVTALEKLHAGKVRDEGRVEIPIHDGHSFGA 76  
 QY 91 DQROEEYEIISFADTLLSSINOTRLEFHFSGRMASGMEVROTFRMFVVO-FPH---NAT 145  
 DB 77 DQGERVSEIISFADTLLSSINOTRLEFHFSGRMASGMEVROTFRMFVVO-FPH---NAT 145  
 QY 146 QTMNIRLVLPYDTNLTLSQYVVOVNASGYOLLGPEAQAACSGHLTLELVESQV 205



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Db 137 RYRVKRVKVEPFGHGRMDVYERVDLKRSGNHTLPLTEATOLAFERGERRLNDVOCGG 196
Oy 206 AHSLILGWF-----SHRPEVAQVRV-EGKHVRVRGIDCGGSMCCROEFVDFRE 258
Db 197 GQELAVPVVVDPEFESHRRPVVQARIGDSRRHRKRKGLLEDGRTNLCRCROQFIDFL 256
Oy 259 IGMNDWIIQPEGVAMNCTGQCPLHVAHMGISAFHFAVLNLLKANAA-AGTTGKSGCC 317
Db 257 IGMNDWIIAPFTGYGVNCEGSPATLACVPGSASSFHTAVVQYMRGILNPGTV--NSCC 314
Oy 318 VPTSRRLSLLYRDSIVYTDIPDMVVEACGCS 352
Db 315 IPTKLSTMSMLYFDDEVNIVKRDVPMNIVEECGA 349

RESULT 11
ID INHA_PIG STANDARD: PRT: 424 AA.
AC P03970:
DT 23-OCT-1986 (Rel. 02, Created)
DT 23-OCT-1986 (Rel. 02, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Inhibin beta A chain precursor (Activin beta-A chain).
GN INHA.
OS Sus scrofa (Pig):
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:
OC Mammalia: Eutheria: Cetartiodactyla: Suina: Suidae: Sus.
OC NCBI_TaxID=9623:
OX 11
RN 11
RP SEQUENCE FROM N.A.
RC TISSUE-Follicular fluid:
RX MEDLINE=60992207; PubMed=2417121:
RA Mason A.J., Hayflick J.S., Ling N., Esch F., Ueno N., Ying S.-Y.,
  Guillaume R., Malt H., Seeburg P.H.:
  "Complementary DNA sequences of ovarian follicular fluid inhibin show
  precursor structure and homology with transforming growth
  factor-beta."
RT Nature 318:659-663(1985).
RL 12
RN 12
RP SEQUENCE OF 309-323.
RC TISSUE-Follicular fluid:
RX MEDLINE=92355604; PubMed=1644823:
RA Nakamura T., Asashima M., Ito Y., Takio K., Uchiyama H., Molya N.,
  Arizumi T., Yasuiro T., Sugino K., Tiliat K., Sugino H.:
  "Isolation and characterization of native activin B."
RT J. Biol. Chem. 267:16385-16389(1992).
RL 13
RC FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE,
  RESPECTIVELY. THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.
  INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE
  FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,
  GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,
  ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,
  EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR
  SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF
  ACTIVINS.
  -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.
  INHIBIN A IS A DIMER OF ALPHA AND BETA-A.
  INHIBIN B IS A DIMER OF ALPHA AND BETA-B.
  ACTIVIN A IS A HOMODIMER OF BETA-A.
  ACTIVIN B IS A HOMODIMER OF BETA-B.
  ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.
  -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
  -----
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  or send an email to license@isb-sib.ch).
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  EMBL: X03266; CAA27020.1; -.
  PIR: A01393; WPPGBA.

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DR HSSP: P18075; 1BMP.
DR InterPro: IPR002400; CF_cysknott.
DR InterPro: IPR000491; Inhibin_betaA.
DR InterPro: IPR001839; TGF_beta.
DR InterPro: IPR001111; TGFb_N.
DR Pfam: PF00019; TGF-beta; 1.
DR Pfam: PF00688; TGF-beta; 1.
DR PRINTS: PR00438; GFCYSKNOT.
DR PRINTS: PR00670; INHIBINB.
DR ProDom: PD000357; TGF-beta; 1.
DR SMART: SM00204; TGFb; 1.
DR PROSITE: PS00250; TGF_BETA_1; 1.
KW Growth factor; Hormone; Glycoprotein; Signal.
FT SIGNAL 1
FT PROPEP 21 308
FT CHAIN 309 424
FT DISULFID 312 320
FT DISULFID 319 389
FT DISULFID 348 421
FT DISULFID 352 423
FT DISULFID 388 388
FT CARBOHYD 165 165
SO SEQUENCE 424 AA; 47476 MW; 436BC2226FDAF52 CRC64;

Query Match 29.48; Score 543; DB 1; Length 424;
Best Local Similarity 31.6%; Pred. No. 6,6e-43;
Matches 133; Conservative 67; Mismatches 141; Indels 80; Gaps 11;

Oy 6 LALLFLPTTVVANKTG-----PCPACWGAIF--DLESQRELLDLAKKSLIDKLHS 58
Db 10 LASCWIIIVRSPPFGSGHSAAPDCSCALATLPKDVNSOPENVEAVKHTLLNHLK 69
Oy 59 QRPILSRPVSGALKTALQRLR-----GPRRETLLEHDOREVEEIIISF 102
Db 70 KRPDYTVPPKALLNAIRKLHVKGKGVNGYVELEDITRRREM--NELMEQTSIIITF 126
Oy 103 ADTDLSSINQRLLEPHFGSGMAHGEVROTRPMFVQFPH-NATQT-MNIRVL----- 153
Db 127 AEAGTA---RKLRFREISGEGSDLSVERAEIWLFLKVPKANTRFKVSRILEPQOORPQ 183
Oy 154 -----VLRPYDNLTLTSQYVYVYVNASGKQLLGGPAQAACSGHITLLEYPE 202
Db 184 GSADGEAEADGVPEEKESEVLISEKVDARKSTWHIFVSSSIQGLDQKSAIDIRTA 243
Oy 203 SQVAH-----SLILG-----WFSRPFVAQVR--VEGKH 231
Db 244 GEQCHETGASLVLLKKKKKEEBAESKRKDGEGACGVDEKEQSHRFLMLQAROSEHPH 303
Oy 232 RVRRCIDCGGSGSMCCROEFVDFREIGMNDWIIQPEGVAMNCTGQCPLHVAHMGIS 291
Db 304 RRRRGLEDGKVNICCKKQFVSPFDIGMNDWIIAPSGHANVAGECSHLAGTSGSS 363
Oy 292 ASFTAVLVNLLKANAAAGTTGSGCCVPTSRRLSLLYRDSIVYTDIPDMVVEACG 351
Db 364 LSFHSTVINHYMRGRHSPANLKSCTVPTKLPRMSMLYDDQNIKKIDIONMIVEECG 423
Oy 352 S 352
Db 424 S 424

RESULT 12
ID INHA_HUMAN STANDARD: PRT: 426 AA.
AC P08476; Q14599;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Inhibin beta A chain precursor (Activin beta-A chain) (Erythroid
  differentiation protein) (EDF).
GN INHA.
OS Homo sapiens (Human).
OC Eukaryota: Metazoa: Chordata: Vertebrata: Euteleostomi:

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OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID:9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-60186863; PubMed-3754442;  
 RA Mason A.J., Niall H.D., Seeburg P.H.;  
 RT "Structure of two human inhibins.";  
 RL Blochem. Biophys. Res. Commun. 135:957-964(1986).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-80190086; PubMed-3267209;  
 RA Murata M., Eto Y., Shibai H., Sakai M., Muramatsu M.;  
 RT "Erythroid differentiation factor is encoded by the same mRNA as that  
 of the inhibin beta A chain.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 85:2434-2438(1988).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-92135888; PubMed-1777673;  
 RA Tanimoto K., Handa S.I., Ueno N., Murakami K., Fukunizu A.;  
 RT "Structure and sequence analysis of the human activin beta A subunit  
 gene.";  
 RL DNA Seq. 2:103-110(1991).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX Glossip D., Dubuque T., Duckles G.;  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE OF 311-426 FROM N.A.  
 RX MEDLINE-87005283; PubMed-3758355;  
 RA Stewart A.G., Milborrow H.M., Rling J.M., Crowther C.E., Forge R.G.;  
 RT "Human inhibin genes. Genomic characterisation and sequencing.";  
 RL FEBS Lett. 206:329-334(1986).  
 RN [6]  
 RP SEQUENCE OF 311-426 FROM N.A.  
 RC TISSUE-Testis;  
 RA Berg H., Walter M., Northmann W.;  
 RL Submitted (MAY-1993) to the EMBL/GenBank/DBJ databases.  
 CC [1-] FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC [1-] SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC [1-] SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: M13436; AAA59168.1; -  
 DR EMBL: X04447; CAA28041.1; -  
 DR EMBL: X57578; CAA40805.1; -  
 DR EMBL: X57579; CAA40805.1; JOINED.  
 DR EMBL: X57579; CAA40805.1; -  
 DR EMBL: AC005027; AAD43185.1; -  
 DR EMBL: J03634; AAA3787.1; -  
 DR EMBL: A14422; CAA01159.1; -  
 DR EMBL: X72498; CAA51163.1; -  
 DR PIR: A30884; A30884.  
 DR PIR: B24248; B24248.

DR PIR: B23556; B23556.  
 DR PIR: S30488; S30488.  
 DR HSSP: P18075; IBM.  
 DR MIM: 147290; -  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR000491; Inhibin\_betaA.  
 DR InterPro: IPR001839; TGF\_beta.  
 DR InterPro: IPR001111; TGF\_beta.  
 DR Pfam: PF000019; TGF\_beta; 1.  
 DR Pfam: PF00688; TGF\_beta; 1.  
 DR PRINTS: PR00438; GRCYSKNOT.  
 DR PRINTS: PR00670; INHIBINB.  
 DR ProDom: PD000357; TGF\_beta; 1.  
 DR SMART: SM00204; TGF\_beta; 1.  
 DR SMART: PS00250; TGF\_beta; 1.  
 DR Growth factor: Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1 20  
 FT PROPEP 21 310  
 FT CHAIN 311 426  
 FT DISULFID 314 322  
 FT DISULFID 321 391  
 FT DISULFID 350 423  
 FT DISULFID 354 425  
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 FT CARBOHYD 165 165  
 FT CONFLICT 377 379  
 FT SEQUENCE 426 AA; 47442 MW; 201CDEDF9C8B6919 CRC64;  
 Query Match 29.28; Score 540; DB 1; Length 426;  
 Best Local Similarity 31.28; Pred. No. 1,3e-42;  
 Matches 132; Conservative 70; Mismatches 139; Indels 82; Gaps 11;

QY 6 LIALFLPTPTVYNPKTEG-----PCPACGATF--DLEQRELLDLAKSITDKLHS 58  
 DB 10 LASCWIVYRSPPTPSGEHSAAPDCPCALALPKDVPNSQPMVAKKHILNMHLK 69  
 QY 59 QREILSPVSRGALKTALQRLR-----GPRRELLBHDQREYEIISF 102  
 DB 70 KRDPVQVPKALMLAKRLHKGKNGENYVELEDIGRAEH--NELMEOTSEIITF 126  
 QY 103 ADTLDSSINOTRLEFHSGMASGMEVQTRFMFQVPPH-NATOT-MNIRVILVLR-- 158  
 DB 127 AE---SGTARKTLHFETISREGSOLSYERAEMVFLKVPKANKRTRVTYIRLFGQCKHPQ 183  
 QY 159 -----DINLTLSQYVYVGNASGWQLLIGPEQAACSGHLLTEL--- 199  
 DB 184 GSLDTGEAEVGLKGERSELLSEKVVQARKSTWHFVPSSTIORLLDQKSSLDVRIA 243  
 QY 200 VPEQVANSLLT-----GMFSHRPFVAQVR--VEG 229  
 DB 244 CQCCQSGASVYLKCKKKKEEGEKKKGGCGAGADEEKQSHRPFLMLQAROSEDH 303  
 QY 230 KRRVRRRGIDCGGSRMCCROGEFVDFREIGNWDWITOEFGYAMNCTGCPPLHVAGMP 289  
 DB 304 PRRRRRGLECCGKVNICKKQEFVSKDIGMNDWILIPAGYANVCCEGCPHINACTSG 363  
 QY 220 ISASHTAVLNLKANKANAAGTGGSCVPTSRRLPLSLYYDRDSNINVKTDIDMVEAC 349  
 DB 364 SLSFHSYVINYRMRGHSFPANLKSQVPTKLRPWSMLYYDDQGNLIKIDQNMITYECC 423  
 QY 350 GCS 352  
 DB 424 GCS 426  
 RESULT 13  
 ID INHA\_MOUSE STANDARD: PRT: 424 AA.  
 AC Q04998;  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhibin beta A chain precursor (Activin beta-A chain).

GN INHBA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 ON NCBL\_TaxID=10090;  
 RX MEDLINE=93321614; PubMed=8330535;  
 RA Albano P.M., Groome N., Smith J.C.;  
 RT "Activins are expressed in preimplantation mouse embryos and in ES  
 and EC cells and are regulated in their differentiation.";  
 RL Development 117:711-723(1993).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
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 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC -1- TISSUE SPECIFICITY: UTERUS, OVARY, AND LIVER.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: X69619; CAA49325.1; -  
 DR PIR: S31440.  
 DR HSP: P18075; IBMP.  
 DR MGD: MGI:96570; Inhba.  
 DR InterPro: IPR002400; GF\_cysknob.  
 DR InterPro: IPR000491; Inhbin\_betaa.  
 DR InterPro: IPR001839; TGF\_beta.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam: PF00019; TGF\_beta.1.  
 DR Pfam: PF00688; TGF\_beta\_propeptide.1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRINTS: PR00670; INHIBINBA.  
 DR ProDom: PD000357; TGF\_beta.1.  
 DR SMART: SM00204; TGFb.1.  
 DR PROSITE: PS00250; TGF\_BETA.1; 1.  
 KM Growth factor; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1 20  
 FT PROPEP 21 308  
 FT CHAIN 309 424  
 FT DISULFID 312 320  
 FT DISULFID 319 389  
 FT DISULFID 348 421  
 FT DISULFID 352 423  
 FT DISULFID 388 388  
 FT CARBOHYD 165 165  
 SQ SEQUENCE 424 AA: 47392 MW: 80C251B8754A7213 CRC64;  
 Query Match 29.1%; Score 538; DB 1; Length 424;  
 Best Local Similarity 32.1%; Pred. No. 1.9e-42;  
 Matches 136; Conservative 68; Mismatches 134; Indels 86; Gaps 14;  
 OY 6 LIALFLPTTTPVKNPKTEG-----PCPACWGAIRDL-----ESQRELLDLAKKSLIDL 55  
 DB 10 LLASCMITVRSPTPSGSGSAPDCPSC--ALATLPKDGNSQPF-MVEAVKHLHML 66

OY 56 HLSQRPILSRPVSRGALKTALQRLR-----GPRRETLLEHDOREYEI 99  
 DB 67 HLKRRDPVQPVRAALLNATRLHVGKGVENGVEIEDDIBRAEM--NELMPTSEI 123  
 OY 100 ISFADDDLSINOTRLEFHSGRNASGMEVROTREFYQFPH-NATQI-MNIRVLVLR 157  
 DB 124 ITPAE--SGTARKTLHFELSKESGDSLSVERAEVWLFIKVPKANTRTKVTIRLQOQK 180  
 OY 158 Y-----DNNLTLSQYVQVNVASGQQLLGPEAQAACSGHITL 199  
 DB 181 HPGCSLDTGDAEEMGKGERSELSLSEKVDARKSTWIEIFPVSSIQRLDQKSLDV 240  
 OY 200 ---VPESOVAHSSLT-----GWF-----SHRPFAAQR--VE 228  
 DB 241 RICEOCESASLVLGKKKKKEYDGKKDGGGEEKEGSHRPFMLQANQSED 300  
 OY 229 GKRRVRRRGIDCQSGSRMCQEFVDERLGWDMIIQPEGYAMNCTGOCPLHYAGP 288  
 DB 301 HPHRRRRRGLECDKRVNICKKQFVSFKIDGMWMIIPSGYHANYCGEGCSHLAGTS 360  
 OY 289 GISASFHTAVLNLKANAAGTGRGCCVPTSRRLSLTYDRDSNIYKTDIPDMVYA 348  
 DB 361 GSSLFSFSTVINHYRMGHSFPAANKSCVPFKLRPMMLYDDGQNIKKDIQNMIVEE 420  
 OY 349 CGCS 352  
 DB 421 CGCS 424  
 RESULT 14  
 ID INHBA\_RAT STANDARD: PRT: 424 AA.  
 AC P18331;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Inhbin beta A chain precursor (Activin beta-A chain).  
 GN INHBA.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 ON NCBL\_TaxID=10116;  
 RX MEDLINE=91042598; PubMed=3153478;  
 RA Woodruff T.K., Meunier H., Jones P.B.C., Hsueh A.J.W., Mayo K.E.;  
 RT "Rat Inhbin: molecular cloning of alpha- and beta-subunit  
 complementary deoxyribonucleic acids and expression in the ovary.";  
 RL Mol. Endocrinol. 1:561-568(1987).  
 CC -1- FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HYPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC EMBRYONIC DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC -1- SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----

CC EMBL: M37482; AAA1436.1; -  
 DR PIR; B40056; B40056.  
 DR HSSP; P18075; IAMP.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR000491; Inhibin\_beta.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF\_beta\_propeptide; 1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRINTS: PR00670; INHIBINBA.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF\_BETA\_1; 1.  
 DR Growth factor; Hormone; Glycoprotein; Signal.  
 FT SIGNAL 1 20  
 FT PROPEP 21 308  
 FT CHAIN 309 424 INHIBIN BETA A CHAIN.  
 FT DISULFID 312 320 BY SIMILARITY.  
 FT DISULFID 319 389 BY SIMILARITY.  
 FT DISULFID 348 421 BY SIMILARITY.  
 FT DISULFID 352 423 BY SIMILARITY.  
 FT DISULFID 388 388 INTERCHAIN (BY SIMILARITY).  
 FT CARBOHYD 165 165 N-LINKED (GLCNAC... ) (POTENTIAL).  
 SQ SEQUENCE 424 AA; 47406 MW; B2DAF917FA50984 CRC64;

Query Match 29.1%; Score 538; DB 1; Length 424;  
 Best Local Similarity 32.1%; Pred. No. 1.9e-42;  
 Matches 136; Conservative 66; Mismatches 134; Indels 86; Gaps 14;

OY 6 LLALELPTTVVNPKEG-----PCPACGCAIFD-----ESQRELLDLAKSLDKL 55  
 DB 10 LLAACWIVKSSPTPGSEGHADPCPC--ALATLPKDGPRNSQEP--WEAVKHHLLNML 66  
 OY 56 HLSQRLSPVSRGALKALQRLR-----GPRRTLEHDOQEYEI 99  
 DB 67 HLRKRDVYQVPVKAALINIRKLHVCKVGENGYEIEDIDIRRAEM---NEIMEQTSI 123  
 OY 100 ISPAOTDLSSINOTRLEFHFSGRMAQMEVROTREFVQFPH--NATOT--MIRIVLVRP 157  
 DB 124 ITFAE---SCTARKTLHFETSKESDLSVVERAEWMLFLKPKARTKRYIRLQOQK 180  
 OY 158 Y-----DTNLTLSQYVQVNAQVQLLGPQAACSGHLLLEL 199  
 DB 181 HQGSLMDQDEAEEMGLKGRSELLSEKVVADAKRSTHIFVSSIQGLLDQKSLDV 240  
 OY 200 ---VPESQVAHSSLIL-----GWF-----SHRPFAVAOVR--VE 228  
 DB 241 RIACEQCEQSGASLVLLGKKKKKEVDGDKKSDGGLLEEKEQSHRFLMLQANQSD 300  
 OY 229 GKHRRVRRGIDCGGSMCCROEFFVDFREIGANDWIIQPGYANMFTGQCPPLAVAGMP 288  
 DB 301 HPHRRRRRGLECGKYNVICCKKOFVSEKIDIGMDWIIAPSGYHANYCEGECPSHAGTS 360  
 OY 289 GISASHTAVLNLKNAAGAGTGRCSCVPTSRPLSLLYADRSNIVYKTIIPQVVA 348  
 DB 361 GSSLASHSVIVINRYRARGHSPANLAKSCVPTKLRPMMLTYDDGONITIKDIONIVEE 420  
 OY 349 CGCS 352  
 DB 421 CGCS 424

RESULT 15

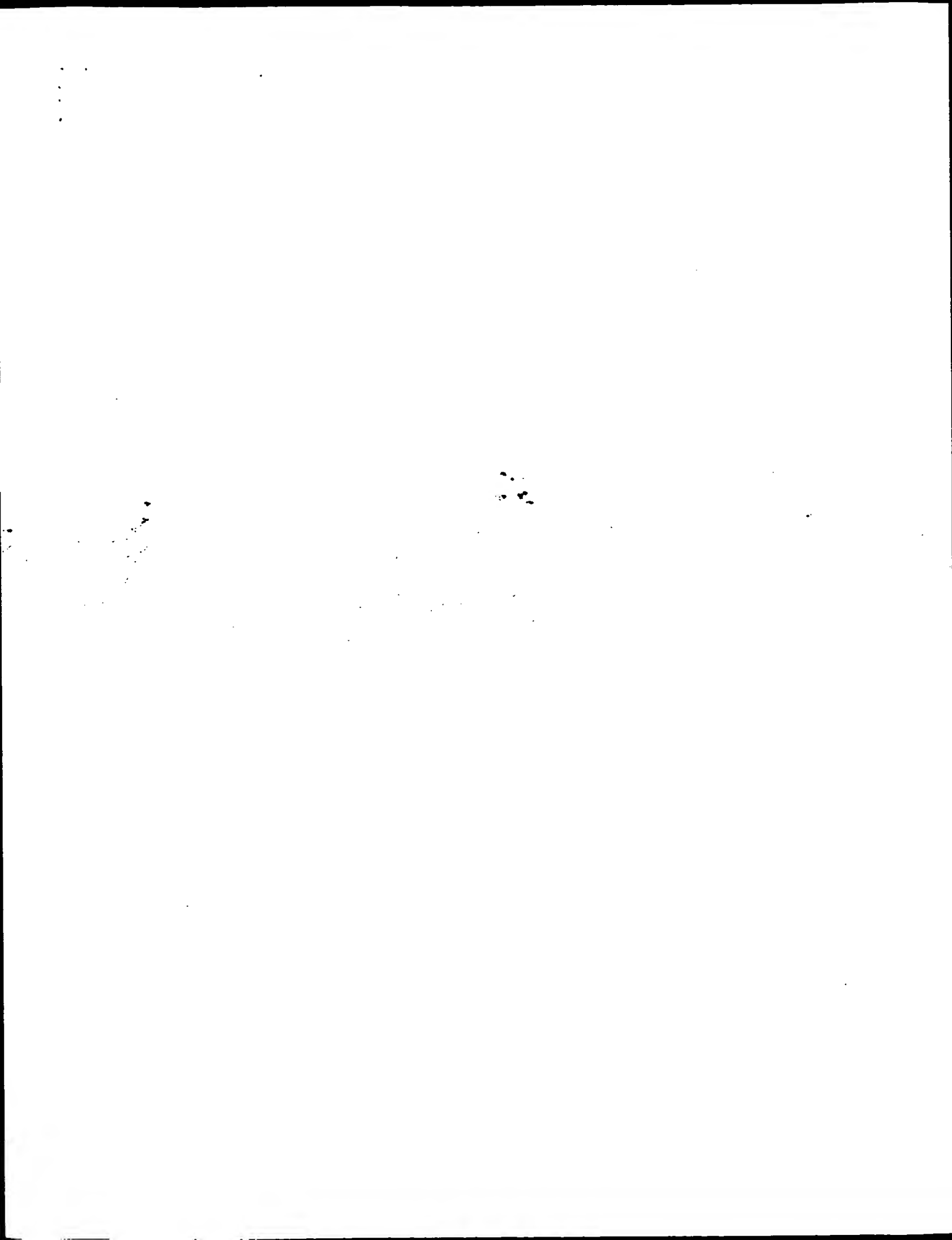
ID ID\_HORSE STANDARD: PRT: 426 AA.  
 AC P55102;  
 DT 01-OCT-1996 (rel. 34, Created)  
 DT 01-OCT-1996 (rel. 34, Last sequence update)  
 DT 16-OCT-2001 (rel. 40, Last annotation update)  
 DE Inhibin beta A chain precursor (Activin beta-A chain).  
 GN INHBA..

OS Equus caballus (Horse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.  
 OX NCBI\_TaxID=9796;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Ovary;  
 RX MEDLINE=96031670; PubMed=7548399;  
 RA Yoshida S., Yamanouchi K., Hasegawa T., Ikeda A., Suzuki M.,  
 Chang K., Matsuyama S., Nishihara M., Takahashi M.,  
 \*Molecular cloning of cDNA for equine ovarian Inhibin/activin beta A  
 subunit.\*  
 RT J. Vet. Med. Sci. 57:469-473(1995).  
 CC - FUNCTION: INHIBINS AND ACTIVINS INHIBIT AND ACTIVATE.  
 CC RESPECTIVELY, THE SECRETION OF FOLLITROPIN BY THE PITUITARY GLAND.  
 CC INHIBINS/ACTIVINS ARE INVOLVED IN REGULATING A NUMBER OF DIVERSE  
 CC FUNCTIONS SUCH AS HIPOTHALAMIC AND PITUITARY HORMONE SECRETION,  
 CC GONADAL HORMONE SECRETION, GERM CELL DEVELOPMENT AND MATURATION,  
 CC ERYTHROID DIFFERENTIATION, INSULIN SECRETION, NERVE CELL SURVIVAL,  
 CC EMBRYONIC AXIAL DEVELOPMENT OR BONE GROWTH, DEPENDING ON THEIR  
 CC SUBUNIT COMPOSITION. INHIBINS APPEAR TO OPPOSE THE FUNCTIONS OF  
 CC ACTIVINS.  
 CC - SUBUNIT: DIMERIC, LINKED BY ONE OR MORE DISULFIDE BONDS.  
 CC INHIBIN A IS A DIMER OF ALPHA AND BETA-A.  
 CC INHIBIN B IS A DIMER OF ALPHA AND BETA-B.  
 CC ACTIVIN A IS A HOMODIMER OF BETA-A.  
 CC ACTIVIN B IS A HOMODIMER OF BETA-B.  
 CC ACTIVIN AB IS A DIMER OF BETA-A AND BETA-B.  
 CC - SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 CC -----  
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 CC -----

Query Match 28.9%; Score 534; DB 1; Length 426;  
 Best Local Similarity 31.2%; Pred. No. 4.6e-42;  
 Matches 132; Conservative 68; Mismatches 141; Indels 82; Gaps 11;  
 OY 6 LLALELPTTVVNPKEG-----PCPACGCAIF--DLSQRELLDLAKSLDKLILS 58  
 DB 10 LLAACWIVKSSPTPGSEGHADPCPCALATLPKDGPRNSQEP--WEAVKHHLLNMLHLK 69  
 OY 59 ORPLSRVSRGALKALQRLR-----GPRRTLEHDOQEYEIISF 102  
 DB 67 HLRKRDVYQVPVKAALINIRKLHVCKVGENGYEIEDIDIRRAEM---NEIMEQTSI 123

DB 70 KRPDYTPVPKALLNIRKILHVGKVGNGVEIEDDIGRAEM---NEIMEQTSITTP 126  
OY 103 ADPLSSINOTRLEFHFSGRMASGMEVROTREMFPVOPPH-NATOT-MNIRVLVLRPY-- 158  
DB 127 AE---SGTAKTILHEFISKESSDLSYVERAEVWLFKVPKANRTSKVTIRLLOOQKHPO 183  
OY 159 -----DTNLTLSQYVVQVNASGWYOLLGPEAQACSQGHLELYPE 202  
DB 184 GSSEDTRREAEADLMERSSEQLISEKVVDARKSTWHIFPVSSIQRLDQKSSDIRIA 243  
OY 203 SQVAH---SSLIG-----WFSHRPFVAQVR--VEG 229  
DB 244 CDQCHETGASLVLDGKKKKKEEGEGKKKDGAGAGVDEKEQSHRPFMLQARQSEDH 303  
OY 230 KHRVRRGIDCGSGRMCROEFVDPREIGMNDWIIOPEGYAMNFCCTQCPLHVAQMPG 289  
DB 304 PHRRRRRGLECDCKVNICKKOFVSEFDIGMNDWIIPSGYHANYCEGECPSHIACTSG 363  
OY 290 ISASFHTAVLNLKANAAGTTGRGCCVPTSRRLPLSLYYDRDSNIVKTDJPDWVVEAC 349  
DB 364 SLSFHTSTVINQYRLRGHNPANLKSQCVPTKLRPMMLYDDGONIIKKDIONMIVEEC 423  
OY 350 GCS 352  
DB 424 GCS 426

Search completed: October 12, 2002, 02:06:56  
Job time : 15.5 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: October 11, 2002, 23:57:49 ; Search time 42 Seconds

(without alignments)  
1449.862 Million cell updates/sec

Title: US-09-684-383-4

Perfect score: 1850

Sequence: 1 MASSLLALLFLPTTVNP.....DSNIVKTDIPDMVEACGCS 352

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP tvirus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	699.5	37.8	367	13	Q91696 xenopus lae
2	587.5	31.8	350	11	Q91XN3 mus musculu
3	566.5	30.6	370	11	Q91X30 xenopus lae
4	545.5	29.5	395	13	Q9PWG6 anguilla ja
5	537	29.0	426	4	Q9HBP0
6	533.5	28.8	393	13	Q90261
7	528	28.5	413	13	Q98860
8	527	28.5	392	13	Q98860
9	499	27.0	424	13	Q98860
10	488.5	26.4	404	13	Q98860
11	368	19.9	119	6	Q95KPI
12	367.5	19.9	119	13	Q95KPI
13	367	19.8	119	6	Q95N79
14	367	19.8	119	6	Q95KPI
15	357	19.3	138	13	Q9W6T9
16	356	19.2	115	13	Q9DGF1

17	356	19.2	115	13	Q9DGE9	Q9d99 cyprinus ca
18	356	19.2	115	13	Q9DGE6	Q9d96 oryza lat
19	350	18.9	115	13	Q9DGE0	Q9d90 cyprinus ca
20	341	18.4	115	13	Q9DGE7	Q9d97 oryza lat
21	334	18.1	115	13	Q9DGE2	Q9d92 cyprinus ca
22	331.5	17.9	115	13	Q9DGE9	Q9d99 cyprinus ca
23	331.5	17.9	115	13	Q9DGE8	Q9d98 cyprinus ca
24	331	17.9	115	13	Q9DGE8	Q9d98 cyprinus ca
25	330.5	17.9	115	13	Q9DGE8	Q9d98 cyprinus ca
26	325	17.6	115	13	Q9DGE8	Q9d98 cyprinus ca
27	324.5	17.5	115	13	Q9DGE8	Q9d98 cyprinus ca
28	322.5	17.4	115	13	Q9DGE8	Q9d98 cyprinus ca
29	322	17.4	115	13	Q9DGE8	Q9d98 cyprinus ca
30	321	17.4	115	13	Q9DGE8	Q9d98 cyprinus ca
31	318	17.2	115	13	Q9DGE8	Q9d98 cyprinus ca
32	317	17.1	115	13	Q9DGE8	Q9d98 cyprinus ca
33	314.5	17.0	115	13	Q9DGE8	Q9d98 cyprinus ca
34	313.5	16.9	115	13	Q9DGE8	Q9d98 cyprinus ca
35	310	16.8	115	13	Q9DGE8	Q9d98 cyprinus ca
36	309.5	16.7	115	13	Q9DGE8	Q9d98 cyprinus ca
37	306.5	16.6	115	13	Q9DGE8	Q9d98 cyprinus ca
38	300.5	16.2	115	13	Q9DGE8	Q9d98 cyprinus ca
39	295.5	16.0	115	13	Q9DGE8	Q9d98 cyprinus ca
40	288	15.6	115	13	Q9DGE8	Q9d98 cyprinus ca
41	287	15.5	115	13	Q9DGE8	Q9d98 cyprinus ca
42	286	15.5	115	13	Q9DGE8	Q9d98 cyprinus ca
43	285	15.4	115	13	Q9DGE8	Q9d98 cyprinus ca
44	283.5	15.3	115	13	Q9DGE8	Q9d98 cyprinus ca
45	283	15.3	115	13	Q9DGE8	Q9d98 cyprinus ca

## ALIGNMENTS

## RESULT 1

Q91696 ID Q91696 PRELIMINARY; PRT; 367 AA.  
AC Q91696;  
DT 01-NOV-1996 (TRENBLER, 01, Created)  
DT 01-NOV-1996 (TRENBLER, 01, Last sequence update)  
DT 01-DEC-2001 (TRENBLER, 19, Last annotation update)  
DE ACTIVIN D PRECURSOR.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;  
OC Xenopodidae; Xenopus.  
OX NCBI\_TaxID=8355;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TRISUB-LIVER.  
RX MEDLINE=95275314; PubMed=7755637;  
RA Oda S., Nishimatsu S., Murakami K., Ueno N.;  
RT "Molecular Cloning and functional analysis of a new activin beta  
subunit: a dorsal mesoderm-inducing activity in Xenopus.";  
RL Biochem. Biophys. Res. Commun. 210:581-588(1995).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: D49543; BAA08494.1; -;  
DR HSSP: P12643; 3BMP.  
DR InterPro: IPR002400; GF\_cysknot.  
DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGFb\_N.  
DR Pfam: PF00019; TGF-beta; 1.  
DR Pfam: PF00688; TGF-beta; 1.  
DR PRINTS: PR00438; GFCYSKNOT.  
DR ProDom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.  
DR PROSITE: PS00250; TGF-BETA; 1.  
KW Glycoprotein; Signal.  
FT SIGNAL 1 253  
FT CHAIN 254 367 POTENTIAL.  
SQ SEQUENCE 367 AA; 41729 MW; C7E6334BD06FA04 CRC64;  
Query Match 37.8%; Score 699.5; DB 13; Length 367;



Best Local Similarity 39.3%; Pred. No. 1,1e-61;  
Matches 145; Conservative 65; Mismatches 122; Indels 37; Gaps 7;

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OY 6 LLLALLFTPTVYVNPKEGPCPCACWGAIFLESORELLDLAKSILDKLHLSORPIIS 65
DB 14 LTLTLAGALASTOGLTKKSCPCSCG-----VODKEVATLEAKOOLTKLHKEPNITH 67
OY 66 PVSRCALKTALOR--LRGRRETLL-----EHDQROEYEIISFADTSSINOT 113
DB 68 PVPKCAVANAALRLHLNKPMEGLFGSNDMSNTENTDTDOQSYEIIISFAEYEYINENSI 127
OY 114 RLEPHFSGMAASGEVROTRFMPFVOPFHATOTMIRVLVLRPYDTNLTLTSQYVOVN 173
DB 128 TLNFOFTREKESAHVLAQALMLFFKANRTISOQNETTLVLYOEAYSRRILSEKLEPR 187
OY 174 ASGWYOLLGPEQAACSCGHTLEL-----VPESQVASHLLIGWFSHREPVAAO 224
DB 188 WFGWOTFSLSKSMLOTFEPDGKNSLOLELNCDCODVPLANPN-----SHOPLVAVO 240
OY 225 VAV-EGKHVRARRIGIDCGGSRMCROEFVDFREIGWMDNIIOPEGYAMNFCGCPH 283
DB 241 AVHSHSHATKSLNCDONSICRDYVDFIDGMDMIKEGVOINCMGLCPMH 300
OY 284 VAGMPCISAFHTAVNLKANAAGTTGSGCCVPTSRRLSLLYDRDSNIYKTDIPD 343
DB 301 IAGAPCMAAFHTVNLTKANNI--OTAVNSCCVPTKRRLSLMLYFRNNNVLTDIAD 358
OY 344 MYVEACGCS 352
DB 359 MIVEACGCS 367

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## RESULT 2

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OY 091XH3 PRELIMINARY: PRT: 350 AA.
AC 091XH3;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DB 1NHBIN BETA E.
OS Mus musculus (Mouse).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN 111
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC010404; AAH10404.1; -
SQ SEQUENCE 350 AA; 39002 MW; 9B7EA8AFAC389FA CRC64;

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Query Match 31.8%; Score 587.5; DB 11; Length 350;  
Best Local Similarity 38.0%; Pred. No. 1.8e-50;  
Matches 141; Conservative 66; Mismatches 109; Indels 55; Gaps 14;

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OY 5 LLLALLFTPTVYVNPKEGPCPCACWGAIFLESORELLDLAKSILDKLHLSORPIIS 64
DB 12 LLMALVWV-----OSTRSACPCGCGPTLAPOGERRALVLELAKOOLLEGHLTSRPRIT 64
OY 65 RPSRSKALKTALORLRPR-----RETLLEHDQROEYEIISFAD--TDLSSINOTRLE 116
DB 65 RPLQALALTRALRLLO--PKSNVPGNRE-----KVISFATIIDKSTSTYSRMTL 111
OY 117 FHSCHMASGMEVROTRFMEFVOPFHATOTMIRVLVLRPYDTNL-----TLTSQYVOVN 172
DB 112 FOLSPILMSHNL-----YHARLMLNVPSPFGTLYLR--IFRCCTTRCGRGTPLAEH--QT 163
OY 173 MASGWYOLLGPEQAACSCGHTLEL-----VPESQVASHLLIGWF-SHREPVAAOV 225
DB 164 TSSGMWALTLTPSSGLRSBEDSCVAVLQLEFRPLDINSTAAGLPRLLDLTGAQGRPLLEKRI 223
OY 226 RVE--GKHVRARRIGIDCGGSRMCROEFVDFREIGWMDNIIOPEGYAMNFCGCPH 283

```

DB 224 RANPEGAGARRRRPTCEPTEPLCCRDHYVDFOLGKMDWILQPSYQLNYCSGGCPH 283

OY 284 VAGMPCISAFHTAVNLKANA--AAGTTGRSCCVPTRRLSLLYDRDSNIYKTDI 341  
DB 284 LAGSPGIASHASHAVSLKANNPAGS-----SCCVPTARRRLSLLYLDHNGVYATDV 339

OY 342 PDVVEACGCS 352  
DB 340 PDVVEACGCS 350

## RESULT 3

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OY 091350 PRELIMINARY: PRT: 370 AA.
AC 091350;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE ACTIVIN BETA B SUBUNIT.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN 111
RP SEQUENCE FROM N.A.
RX MEDLINE=93273083; PubMed=8500654;
RA Doehmann C.E., Hemmati-Briyanlou A., Thomsen G.H., Fields A.,
RA Woolf T.M., Melton D.A.;
RT "Expression of activin mRNA during early development in Xenopus
RT laevis."
RL Dev. Biol. 157:474-483(1993).
CC -!- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.
DB EMBL: S61773; AAB26863.1; -.
DB HSSP: P18075; IBM.
DB InterPro: IPR002400; GF_cysknol.
DB InterPro: IPR001839; TGF-beta.
DB InterPro: IPR001111; TGFb.N.
DB Pfam: PF00019; TGF-beta.1.
DB Pfam: PF00688; TGFb-propeptide.1.
DB PRINTS: PR00438; GFCYSKNOT.
DB PRODOM: PD000357; TGF-beta.1.
DB SMART: SM00204; TGFb.1.
DB PROSITE: PS00250; TGF-BETA.1.
KW Glycoprotein.
SQ SEQUENCE 370 AA; 41679 MW; AD2150ZAC45FIDE9 CRC64;

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Query Match 30.6%; Score 566.5; DB 13; Length 370;  
Best Local Similarity 34.7%; Pred. No. 2.5e-48;  
Matches 130; Conservative 73; Mismatches 137; Indels 35; Gaps 12;

```

OY 5 LLLALLFTPTVYVNPKEGPCPCACWGAIFLESORELLDLAKSILDKLHLSORPI 62
DB 4 LLLPGLLAGLARTCAPSPPEPCPCCHP---PMEPR---MLEAVKRIHLLTLHMDRPN 57
OY 63 LSRPVSRAKLTALORLRPR--RE-----TLLEHD-----QROEYEIISFADTDL 108
DB 58 ITHVPRAMVASALRLKLGAVREEDNLEIPDLGHSLLPPCHSTENSALIELTFAETDGV 117
OY 109 SINQRLRLEPHFSGMAASGEVROTRFMPFVOPFH--NATOTMIRVLVLRPYDTNLTL 165
DB 118 TASRRLRLEFTTINEGNQLNLFVQSNLMVLKLEVDMDKSRKRIKHYFOAFNPDKNM 177
OY 166 SQYVQVAVASGWYOLLGPEQAACSCG--HTLLELVPEQVASHLSL-----GWFSHRP 219
DB 178 VEKKDIRSGHHTPPLTALISLFEGERKRLNLEVOCDGCGESVYIPVYDPPDESHRP 237
OY 220 FVAAGVAV-EGKHVRARRIGIDCGGSRMCROEFVDFREIGWMDNIIOPEGYAMNFCG 278
DB 228 FLVVAHARLADNKHRLRKRGLECDGHNTLCCROQFYDFRLIGWMDWIIAPAGYGVNCEG 297
OY 279 OCPHVAAGMPCISAFHTAVNLKANA--AGTTGSGCCVPTSRRLSLLYDRDSNIY 337

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Db 298 SCPAYLACVPSASSPHTAVNOYMRGLNPGTV--NSCCIPTKLSMMLYFDEYNIV 355  
 QY 338 KTDIPDMVVEACGCS 352  
 Db 356 KRDVPMNIVECCGA 370

## RESULT 4

Q9PMG6 PRELIMINARY: PRT: 395 AA.  
 AC Q9PMG6  
 DT 01-MAY-2000 (Tremblrel. 13, Created)  
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ACTIVIN B.  
 OS Anguilla japonica (Japanese eel).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;  
 OC Anguillidae; Anguilla.  
 OX NCBI\_Taxid=7937;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=TESTIS;  
 RA Mura T., Mura C., Eto Y., Nagahama Y.;  
 RT "Activin B gene is required for the initiation of spermatogenesis in  
 the Japanese eel, Anguilla japonica."  
 RL Submitted (MAR-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AB025356; BAA83804.1; -  
 DR HSSP: P12643; 38MP.  
 DR InterPro: IPR000381; Inhibin\_beta.  
 DR InterPro: IPR001318; Inhibin\_beta.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR PRINTS: PR00672; INHIBINB.  
 DR PRINTS: PR00672; INHIBINB.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 DR GlycoProtId: -  
 SO SEQUENCE 395 AA; 43889 MW; FA56D62D18509A3 CRC64;

Query Match 29.5%; Score 545.5; DB 13; Length 395;  
 Best Local Similarity 32.2%; Pred. No. 3.5e-46;  
 Matches 121; Conservative 78; Mismatches 136; Indels 41; Gaps 11;

QY 14 PTVVNPRTGPPACWGAIFDLESORELL--LDLAKSLDKLHLSORPILSRVSRGA 71  
 Db 24 PGETQTQVSQDTGASC--GLGQPEESGRMDIDLEAVKRIHLNLRNKRERNITPIPKAA 82  
 QY 72 LKTAQLQRLR--CPRR-----TLLEHDQROEYEITISPADTDLSSINQRLRPH 118  
 Db 83 MVALRLKRLHAKKVEDGKVEIPIPLDGHATYNNVEQEDTSEIISPAESD--ELTSSKSSPF 140  
 QY 119 F--SGRASGMEVQTRFMFVQFPFNATQTMNIRVLYLRPY--DTNLTLTS----- 166  
 Db 141 FLISNENONILYVSQASIMLYFRLLPSASEKSRKRYTKVYQQTGAATAAAAAAGRW 200  
 QY 167 ---QYVQVNASGWYOLLGPEAOACSGHLTLLEVPESOVASHSLIL-----GMFSH 217  
 Db 201 GLVEKVELKRSKGMHTFPLTEPRVGVFERGDRQDLVRCGECEAAAVLPVLDVPGDESH 260  
 QY 218 RPPVAAQVRV--EGKRRVRRGIDCGGSMCCROEFVDFREIGNWMIIIOPEGYANMFC 276  
 Db 261 RPFLLVQARLADGKHRIKRRGLECDGTGLCCROGPFYIDFRLLIGMDWMIAPSGYFGNYC 320  
 QY 277 TGOCPLHVAAGMPGISASFHTAVNLILKANAAGCTGRCSCCVTSRRPLSLLYDRDSNI 336  
 Db 321 EGSCPAVMAAGVPSASSPHTAVNOYRMGRMS--PGSMNSCCIPTRLSTYMSMLYFDEYNI 379

QY 337 VKTDIPDMVVEACGCS 352  
 Db 380 VKRDVPMNIVECCGA 395

## RESULT 5

Q9HBP0 PRELIMINARY: PRT: 426 AA.  
 AC Q9HBP0  
 DT 01-MAR-2001 (Tremblrel. 16, Created)  
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE HYPOTHETICAL 47.5 KDA PROTEIN.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel Human cDNA clones with function of inhibiting cancer cell  
 growth."  
 RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: AF218018; AAC17260.1; -  
 DR HSSP: P18075; 1BMP.  
 DR InterPro: IPR002405; Inhibin\_alpha.  
 DR InterPro: IPR000491; Inhibin\_alpha.  
 DR InterPro: IPR001318; Inhibin\_beta.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGF-beta.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGF-beta; 1.  
 DR PRINTS: PR00669; INHIBIN.  
 DR PRINTS: PR00670; INHIBINB.  
 DR ProDom: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGF-beta; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 DR GlycoProtId: Hypothetical protein.  
 SO SEQUENCE 426 AA; 47454 MW; 339276317BD5B408 CRC64;

Query Match 29.0%; Score 537; DB 4; Length 426;  
 Best Local Similarity 31.2%; Pred. No. 2.7e-45;  
 Matches 132; Conservative 69; Mismatches 140; Indels 82; Gaps 11;

QY 6 LLALEFTPTTVVNPRTG-----PCPACWGAIF--DLESORELLDLAKKSLDKLHLS 58  
 Db 10 LLASCWITIVASSPTPGSEBGSAAADPCFSCALALPKVDVPSNPENVEAVKHLNMLHLK 69  
 QY 59 QRPILSRVSRGALKTALQRLR-----GPRRETLLEHDQROEYEITISF 102  
 Db 70 KRPDVIOVPKAAALNIAIRKLHGVKGVGEYVEIEDJGRAM--NLMQTSITLTF 126  
 QY 103 ADPTDLSSINQRLRLEFHSGRASGMEVQTRFMFVQFPN--NATQ--NIRVLYLRPY-- 158  
 Db 127 AE--SGTARKTLHFEISKESGSDLSVERAEVWFLKVPKANRTKTVIRLFOQQRHPQ 183  
 QY 159 -----DTNLTLTSQYVQVNASGWYOLLGPEAOACSGHLTLLE---- 199  
 Db 184 GSLDTEBEAEVGLKGRSELLESEKVVDAKSTWHVEPVSSIORLLDQSSLDVRIA 243  
 QY 200 VPESOVASHSLIL-----GMFSHPPVAAQVR--VEG 229  
 Db 244 CEQCGESGASLIVLKKKKKEEGEGKKKGEGCAGADEKESGHRPPLMLOAKQSEH 303  
 QY 230 KIRVRRRGIDCGGSRKCCROEFVDFREIGNWMIIIOPEGYANMFCGQCPHLHVAAGMP 289  
 Db 304 PHRRRRRGIECDCKVNICCKKQFVSEKIDIGNWMIIAPSGYHANYCEGECPSHLAGTSG 363  
 QY 290 ISASFHTAVNLILKANAAGCTGRCSCCVTSRRPLSLLYIDRDSNIYKTDIPDMVVEAC 349

DB 364 SLSFHSVIVNHYNRHSGSPANLKSVCVPTKLRPMHMLYYDDGONIKKDIQNIYECC 423  
 OY 350 GCS 352  
 DB 424 GCS 426

RESULT 6  
 ID 090261 PRELIMINARY: PRT: 393 AA.

AC 090261: 01-NOV-1996 (Tremblrel. 01, Created)  
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ACTIVIN BETA B.  
 CN INHBB OR ZACHTETAB.  
 OS Brachydanio rerio (zebrafish) (zebra danio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
 OC Cypriniformes; Cyprinidae; Danio.  
 ON NCBI\_TaxID=7955:  
 RP [1]  
 RT SEQUENCE FROM N.A.  
 RX MEDLINE=95011555; PubMed=7926744;  
 RA Wilbrod J., Frederic R.M.;  
 RT "Expression of activin variants: the role of maternal activin."  
 RL Genes Dev. 8:1448-1462(1994).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: X76051; CAA53636.1; -.  
 DR HSSP: P12643; 3BMP.  
 DR ZFIN: ZDB-GENE-990415-2; InhbB.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR PRINTS: PR00438; GFCYSKNOT.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 DR GlycoProtein.  
 SO SEQUENCE 393 AA; 43830 MW; FA769CAD9BEAD252 CRC64;

Query Match 28.8%; Score 533.5; DB 13; Length 393;  
 Best Local Similarity 32.0%; Pred. No. 5; se-45;  
 Matches 124; Conservative 83; Mismatches 139; Indels 41; Gaps 13;

DB 1 MASSLLALLFLPTTVNPKT---ECPCPAC-WGATFDESQRELLDLAKSLDKLH 56  
 DB 13 LSVTLMACLSLVOCSSLAETGSGQVSCGLGHQEDSRMTDFLEAVKRHLNRLQ 72  
 OY 57 LSORPLSHPSRGALKTALQRLG-----PRRETLLHEDROEEY-YETISFAD 104  
 DB 73 MREKNITPIPKANVTALRLKHLACKVREDGRVREINLDSHAHNEQEDELSTISFAE 132  
 OY 105 TDLSSINOTRLEFHSGRMASGMEVROTR-FMFEVOPHNATQTMIRVLV-LRPYDNL 162  
 DB 133 SDDVPSKSLVFLISNEGQNLVLOANLMLYFKLMPGLTEKGLRAKVTVRVHSYERG- 191  
 OY 163 TLTSQVY-----VOVNASGWYOLLGPEAOACSGHLLTLEVPESOVAHSSLLIGW 214  
 DB 192 --GONVHPMKRVELKRSQWHTFPVSEAIRMLAKGGRRDLDIHCECEANVLPJ 248  
 OY 215 F-----SHRPVAAOV-RVEGHRVRRRGIDCGGS-RMCRQEFVDFPREIGNDWI 266  
 DB 249 LVDPSPSRHPLVVAQOQDKHRIKRGLEDCGNGGCLCCROOFYIDFLIGNDWI 308  
 OY 267 OPEGYAMNCTGCPPLHVGMPGISAFHTAVLLILKANA-AAGTTGRGSCVPTSRPL 325  
 DB 309 APAGVYGNCEGSCPAVMAGVPSASSFHTAVVQYRNKRGSPSV--NSCCTPKRLSTM 366

OY 326 SILLYDRDSNVIKTDIPDMVNEACGS 352  
 DB 367 SMLYFDEIVNIVKRDVPMVNEECGA 393

RESULT 7  
 ID 098860 PRELIMINARY: PRT: 413 AA.

AC 098860: 01-FEB-1997 (Tremblrel. 02, Created)  
 DT 01-FEB-1997 (Tremblrel. 02, Last sequence update)  
 DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
 DE ACTIVIN BETA-A SUBUNIT.  
 OS Cynops pyrrhogaster (Japanese common newt).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae; Cynops.  
 ON NCBI\_TaxID=8330;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=TESTIS;  
 RC MEDLINE=96295508; PubMed=8702409;  
 RA Yamamoto T., Nakayama Y., Abe S.;  
 RT "Expression of activin beta subunit genes in sertoli cells of newt  
 testis."  
 RL Biochem. Biophys. Res. Commun. 224:451-456(1996).  
 CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
 DR EMBL: D84516; BAA12693.1; -.  
 DR HSSP: P18075; 1BMP.  
 DR InterPro: IPR002400; GF\_cysknot.  
 DR InterPro: IPR001839; TGF-beta.  
 DR InterPro: IPR001111; TGFb\_N.  
 DR Pfam: PF00019; TGF-beta; 1.  
 DR Pfam: PF00688; TGFb\_propeptide; 1.  
 DR PRINTS: PR00670; INHIBINB.  
 DR PRODOM: PD000357; TGF-beta; 1.  
 DR SMART: SM00204; TGFb; 1.  
 DR PROSITE: PS00250; TGF-BETA; 1.  
 DR GlycoProtein.  
 SO SEQUENCE 413 AA; 46303 MW; 46F6D112A1B010 CRC64;

Query Match 28.5%; Score 528; DB 13; Length 413;  
 Best Local Similarity 31.4%; Pred. No. 2; le-44;  
 Matches 132; Conservative 63; Mismatches 137; Indels 88; Gaps 14;

DB 5 LLLALLFLPTTVNPKREG-----PCPACWGAIDLE-----SQRELLDLAKSLDKL 55  
 DB 10 LLLGLCWIATRASPTTGGGGSVTDQSC--ALGRLKRAADSSQADVNAVKHILSML 67  
 OY 56 HLSORPLSHPSRGALKTALQRL-----RGPRETLLHEDROEEY 97  
 DB 68 HMRSPNITQVPRKALNALIKLHVGVGDGYVEDIDYGRARSELLE-----QTS 122  
 OY 98 EISFADTSLSSINOTRLEFHS-GRMASGME-VROTRFMFEVOP-PHNATQTMIRVLV 154  
 DB 123 EITFAEA-----GSKVLIHEIERSGSDLSVEGAETMLFKLKSNSRTK----LT 173  
 OY 155 LRPY-----DTNLTLSQVYVOVNASGWYOLLGPEAOACSGHLLTLEL 199  
 DB 174 IRLYQOQQRQDERGQRDKKEVLIAEKTLDTRKSGWHTFNIAKSIQHLIDGKTSIDI 233  
 OY 200 -----VPESOVAHSSLLIGW-----WFSHRPP--VAQVVECKHR 232  
 DB 234 RIACDOCEATGATPTLLGKKKKKKEEVKKAANSAGDEERDQSHRPLMIARKEEPIHR 293  
 OY 233 VRRRGIDCGGSRMCRQEFVDFPREIGNDWIIOPEGYAMNCTGCPPLHVGMPGISA 292  
 DB 294 RRRKRGLECDGVSTCKKQPFVSFKDIGNSWIAPGTITANVCBGDCPMTITGTSSGP 353  
 OY 293 SFHTAVLLILKANAAGTTGRGSCVPTSRPLSLLYDRDSNVIVTIDIPDMVNEACGS 352  
 DB 354 SFHAAVTQYRNKRGSPSVTSVASCVCVPTKRLRAMSMLYYDDGONIKKDIQNIYECCGS 413

## RESULT 8

09PMR8 PRELIMINARY: PRT: 392 AA.

AC 09PMR8: 01-MAY-2000 (Tremblrel. 13, Created)

DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE ACTIVIN BETA B SUBUNIT PRECURSOR.

OS Carassius auratus (Goldfish).

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Actinopterygii: Neopterygii: Teleostei: Euteleostei: Ostariophysi: Cypriniformes: Cyprinidae; Carassius.

NCBI\_Taxid=9537;

OK [1]

RN SEQUENCE FROM N.A.

RP TISSUE-Ovary;

RC MEDLINE-97424746; PubMed-9278859;

RA Ge M., Mura T., Kobayashi H., Peter R.E., Nagahama Y.;

RT Cloning of cDNA for goldfish activin beta B subunit, and the expression of its mRNA in gonadal and non-gonadal tissues.\*;

RL J. Mol. Endocrinol. 19:37-45(1997).

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF004669; AAB61468.1; -.

DR HSSP: P12643; 38P.

DR InterPro: IPR000381; Inhibin\_betaB.

DR InterPro: IPR001318; Inhibin\_betaC.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGF-beta.

DR Pfam: PF000019; TGF-beta; 1.

DR Pfam: PF00688; TGF-beta; 1.

DR PRINTS: PR00671; INHIBINB.

DR PRINTS: PR00672; INHIBINB.

DR ProDom: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

DR GlycoProtein; Signal.

KW SIGNAL

FT CHAIN 1 23 POTENTIAL.

FT SIGNAL 1 23 ACTIVIN BETA B SUBUNIT.

SO SEQUENCE 392 AA; 43653 MW; 73AAAT7E1C0B2450B CRC64;

Query Match 28.5%; Score 527; DB 13; Length 392;

Best Local Similarity 33.1%; Pred. No. 2.5e-44;

Matches 120; Conservative 75; Mismatches 129; Indels 38; Gaps 12;

QY 23 EGPPAC-WGAI-FDLESORELLDLAKKSILDKLHLSQRPILSKPVSRGALKTALQIRG 81

DB 37 ESQASCGLGHPDDSGRMDTDLFVAKRHILNLRQMRERPNITPPIKAMVATLRKLA 96

QY 82 -----PRRTLEHNDROEE-YELISFADTDLSSINQTRLEFHSGRMASGMEV 129

DB 97 GKVEDGKVEIPNFGHAHNEVEETSEISFAESDDVPSKSLYFLISNEGNQNLVY 156

QY 130 RQTR-FMEFVOPHINATOTMINRVLV-LRPYDTNLTLSQY-----VQVNASGMYQ 179

DB 157 LQALNLTLYFKLLPGQEGRLKRVYVRSYEG-----CONVHMPMEKRYELKRSQMT 212

QY 180 LLLGPEAQAACSGHLLTLEVESQVANSLLIGWF-----SHRPVAAQV-EVEGKHR 232

DB 213 FVSEAVREMLAKGGRDDLDHCEGCEANVLPILVDPSPSHRPFLVVRQAQADSKHR 272

QY 233 VRRGIDCQG-GSRMCCQOEFFVDFREIGWMDWIIOPEGYAMNFCGTCGLVHAGMPCIS 291

DB 273 IRRKLEDCDNGGLCCGCOFYIDFLIGMDWIIAPAGYGYNCESCPAYMAGVPCSA 332

QY 292 ASFTAVNLKLANA-AAGTTRGSCCVPTSRPLSLTYDRDSNITKTIDIPMVAVEACG 350

DB 333 SSFTAVVNOYRMNGISPSGV--NSCIPTKLSTMSMLYFDDEVINVKRDVPMNIVEECG 390

QY 351 CS 352

DB 391 CA 392

## RESULT 9

098SP9 PRELIMINARY: PRT: 424 AA.

AC 098SP9: 01-JUN-2001 (Tremblrel. 17, Created)

DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)

DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

DE INHIBIN-BETA.

OS Meleagris gallopavo (Common turkey).

OC Eukaryota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi: Archosauria: Aves: Neognathae; Galliformes; Meleagrididae; Meleagris.

NCBI\_Taxid=9103;

OK [1]

RN SEQUENCE FROM N.A.

RP TISSUE-Ovary;

RC Ahn J., You S., Kim H., Foster D.N., El Halawani M.E.;

RT Molecular cloning of turkey inhibin-alpha and beta subunits.\*;

RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.

DR EMBL: AF336338; AAK21265.1; -.

DR HSSP: P18075; 18P.

DR InterPro: IPR002405; Inhibin\_alpha.

DR InterPro: IPR000491; Inhibin\_betaA.

DR InterPro: IPR001318; Inhibin\_betaC.

DR InterPro: IPR001839; TGF-beta.

DR InterPro: IPR001111; TGF-beta.

DR Pfam: PF000019; TGF-beta; 1.

DR Pfam: PF00688; TGF-beta; 1.

DR PRINTS: PR00669; INHIBINA.

DR PRINTS: PR00670; INHIBINA.

DR PRINTS: PR00672; INHIBINB.

DR ProDom: PD000357; TGF-beta; 1.

DR SMART: SM00204; TGF-beta; 1.

DR PROSITE: PS00250; TGF-BETA; 1.

DR GlycoProtein.

SO SEQUENCE 424 AA; 47442 MW; B3E7CF3B9FDF0C59 CRC64;

Query Match 27.0%; Score 499; DB 13; Length 424;

Best Local Similarity 30.4%; Pred. No. 1.8e-41;

Matches 127; Conservative 65; Mismatches 152; Indels 74; Gaps 11;

QY 6 LLLLELPTTVVAPKNEG-----PCPACWGAIF--DLESORELLDLAKKSITDKLHLS 58

DB 10 LTVICWLTIVRSSPTPGSEGHSSVTDCPCALTLTISKDVSSQPEVAVKRNHILNMLHLR 69

QY 59 QRPILSRPVSRGALKTALQIRL-----GPRRTLEHNDROEE-----OEEYETISPADT 105

DB 70 DRNITQPVKRALNMLNINKLHVKGVDGDDGYEIEDDVGRIRQMNVEVETSEITTFAG- 128

QY 106 DLSSINQTRLEFHNS--GRMASGMEVQTRFMFVOPHINATOTMINRVLVLPY----- 158

DB 129 --SGTPKTLHFELISKESSELSVVEHAEWMLFLKYSKANRSRTKVIIRLFQOQROKRG 166

QY 159 -----DTNLTLSQYVYVNASGWYQLLLGPEAQAACSGHLLTEL---VPE 202

DB 187 EGSEDMEDGGLKGRSEFTLISEKAVDTKRTWHIFPVSSSVORLLDQCKSSLDVRIACDL 246

QY 203 SQVAHSSLLI-----GWF-----SHRPVAAQV--VEGKHRV 234

DB 247 COETGASLVLLGKKKKKEDDEGKKEKAGELTGEEEKESHRPFLMLARHSEDRHRR 306

QY 235 RRGIDCGSRMCCQOEFFVDFREIGWMDWIIOPEGYAMNFCGTCGLVHAGMPCISASF 294

DB 307 KRGLCEGCKVNICCKKQFFVSKDIGMSDWIIAPGYHANYEGECPESHAGTSSLSLF 366

QY 295 HTAVNLKLANAAGTTRGSCCVPTSRPLSLTYDRDSNITKTIDIPMVAVEACGS 352

DB 367 HSTVINHYRMGRGSHSPFANLAKSCCVPTKLRPMMLTYDDOONLIKDIOMIYVECCGS 424

RESULT 10

09PW65  
ID 09PW65 PRELIMINARY; PRT: 404 AA.  
AC 09PW65;  
DT 01-MAY-2000 (TREMblrel. 13, Created)  
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE ACTIVIN BETA A PRECURSOR.  
OS Carassius auratus (Goldfish).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Osteichthyes; Osteichthyes;  
OC Cypriniformes; Cyprinidae; Carassius.  
OX NCBI\_TaxID=7957;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN, PITUITARY;  
RA Yam K.M., Yu K.L., Ge W.;  
RT Cloning and characterization of activin beta A subunit.  
RL Mol. Cell. Endocrinol. 0:0-0(1999).  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: AF169032; MAD50448.1;  
DR HSSP: P12643; 3BMP.  
DR InterPro: IPR002405; Inhibin\_alpha.  
DR InterPro: IPR000493; Inhibin\_beta.  
DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001111; TGF-beta.  
DR Pfam: PF00019; TGF-beta; 1.  
DR Pfam: PF00688; TGF-beta; 1.  
DR PRINTS: PR00669; INHIBIN.  
DR PRINTS: PR00670; INHIBIN.  
DR ProDom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.  
DR PROSITE: PS00250; TGF-BETA; 1.  
KM Glycoprotein; Signal.  
FT CHAIN 1 23 POTENTIAL.  
FT SIGNAL 289 404 ACTIVIN BETA A.  
SQ SEQUENCE 404 AA: 44799 MW: 3AFB41B62AB6C6C64;  
Query Match 26.4%; Score 488.5; DB 13; Length 404;  
Best Local Similarity 32.2%; Pred. No. 1.9e-40;  
Matches 119; Conservative 61; Mismatches 142; Indels 47; Gaps 10;

QY 25 PCPACGALFDESQREL-LDLAKKSLDKLHSQRPILSRVSGALKTALQRLGPR 83  
DB 42 PCPSALQROKDSQEDTDWEAVKRRHMLNMLNTRNVTTPVRAALLNIRLHVG 101  
QY 84 -----RETLLEHGORORE--YEIISPADT-DLSSINQRLERHFGSMASME 128  
DB 102 VEEDGTVEEEDGGGEGEHEHQSEOEPEITFAEPDAPDI--MKFDISMEGNTLSVE 159  
QY 129 VQTRFEMFQFPHNATQTMNIRVLYLRPYDTNL-----TLTSQYVQVNASGWYOLL 182  
DB 160 QANVMILLKVAKSRGKGVSVOLQHGKADPGSGADGQEAIVSEKTYDTRSGMHTLV 219  
QY 183 GREAQA-----ACSGHLETLVLP-ESQVASHSLILGFSHRPF--VAA 223.  
DB 220 SRTVQTLDDGSSMLSLRVSCPMCAEAGAVPLIVPTESNKKGR-----EQSHRPLMVL 275  
QY 224 QVRVEGKHVRARRGIDCGSGRMCCROEFVDFREIGNMDWIIQEGYAMNCTGCGPLH 283  
DB 276 KPAEEHPHRSKRGLECDGKIRVCKKQFYVNFKIDGSDWIIARSGYHANYCEGDCPSH 335  
QY 284 VAGMPTISAFHRAVLLKLANAAGTTGRGSCVPTSRRLSLLYDRDSINVKTDIFD 343  
DB 336 VASITSGALSFSHTVINHYRMGRGSPNNIKSCVPTRLRAMSMLYYDEORIKKIDION 395  
QY 344 MVEACGCS 352  
DB 396 MVEECGCS 404

RESULT 11  
Q95KPI PRELIMINARY; PRT: 119 AA.

AC 095KPI;  
DT 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE ACTIVIN SUBUNIT A (FRAGMENT).  
OS Allurus fulgens (Lesser panda).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Carnivora; Fissipedia; Procyonidae; Allurus.  
OX NCBI\_TaxID=9649;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Wang X., Wang Y.;  
RT "Molecular cloning of the activin gene A subunit mature peptide from  
RT panda related animals." to the EMBL/GenBank/DBJ databases.  
RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AY029555; AAK40342.1;  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 119 AA: 13328 MW: 0A319B2F25D83CB6 CRC64;  
Query Match 19.9%; Score 368; DB 6; Length 119;  
Best Local Similarity 51.3%; Pred. No. 4.5e-29;  
Matches 59; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

QY 237 GIDCGSRMCCROEFVDFREIGNMDWIIQEGYAMNCTGCGPLHVGMPGISASFT 296  
DB 3 GLECDGKNVICCKOFVFSFKDIGNMDWIIAPSGYHANYCEGECPSHIACTSGSSLSFHS 62  
QY 297 AVLNLKANAAGTGRGSCVPTSRRLSLLYDRDSINVKTDIPMVVACCC 351  
DB 63 TVINHYRMGRGSPANLKSCVPTRLPMSMLYDDGQNTIKDIONMVECCG 117  
RESULT 12  
ID 042125 PRELIMINARY; PRT: 119 AA.  
AC 042125;  
DT 01-JAN-1998 (TREMblrel. 05, Created)  
DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE ACTIVIN BETA B (FRAGMENT).  
OS Pagrus major (Red sea bream) (Chrysophrys major).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Percoidae;  
OC Sparidae; Pagrus.  
OX NCBI\_TaxID=143350;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Ovary;  
RA Sakakida Y., Kasahara M., Inaba K.;  
RT "Analysis of the activin beta B subunit of Pagrus major.";  
RL Submitted (Aug-1997) to the EMBL/GenBank/DBJ databases.  
CC -1- SIMILARITY: BELONGS TO THE TGF-BETA FAMILY.  
DR EMBL: AB006786; BAA22570.1;  
DR HSSP: P12643; 3BMP.  
DR InterPro: IPR001839; TGF-beta.  
DR InterPro: IPR001839; TGF-beta.  
DR Pfam: PF00019; TGF-beta; 1.  
DR ProDom: PD000357; TGF-beta; 1.  
DR SMART: SM00204; TGF-beta; 1.  
DR PROSITE: PS00250; TGF-BETA; 1.  
KM Glycoprotein.  
FT NON\_TER 1 1  
FT NON\_TER 1 1  
SQ SEQUENCE 119 AA: 13455 MW: EFB0E9E9AD1FA888 CRC64;  
Query Match 19.9%; Score 367.5; DB 13; Length 119;  
Best Local Similarity 50.4%; Pred. No. 5e-29;  
Matches 59; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

QY 226 RVECKHVRARRGIDCGSGRMCCROEFVDFREIGNMDWIIQEGYAMNCTGCGPLHVA 285  
DB 4 QADNRHRIKRGLECDGSSSLCCROQFYIDRLIGNMDWIIAPSGYHANYCEGNCPAYMA 63

OY 286 GMPGASPFHTAVNLKANAAGTTCGSCVPTSRRLPLSLYYDRSDNIVKTDIP 342  
 Db 64 GVPGASPFHTAVNVOYRMGRMS-PGSMNSCIPTKLSTMSLYFDDEYNIVKRDVP 119

## RESULT 13

OY 237 GIDCGGSRMCCROEFFVDFREIGNDWIIIOPEGYAMNFCCTGCPPLHVAGMPCISASFHT 296  
 Db 3 GLECDGKVNICKCKKOFPSFDIGNDWIIAPSGYHANCCEGCPSHIAGTSGSSLSFHS 62

Query Match  
 Best Local Similarity 19.8%; Score 367; DB 6; Length 119;  
 Matches 59; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

OY 237 GIDCGGSRMCCROEFFVDFREIGNDWIIIOPEGYAMNFCCTGCPPLHVAGMPCISASFHT 296  
 Db 3 GLECDGKVNICKCKKOFPSFDIGNDWIIAPSGYHANCCEGCPSHIAGTSGSSLSFHS 62

## RESULT 14

OY 237 GIDCGGSRMCCROEFFVDFREIGNDWIIIOPEGYAMNFCCTGCPPLHVAGMPCISASFHT 296  
 Db 3 GLECDGKVNICKCKKOFPSFDIGNDWIIAPSGYHANCCEGCPSHIAGTSGSSLSFHS 62

Query Match  
 Best Local Similarity 19.8%; Score 367; DB 6; Length 119;  
 Matches 59; Conservative 20; Mismatches 36; Indels 0; Gaps 0;

OY 237 GIDCGGSRMCCROEFFVDFREIGNDWIIIOPEGYAMNFCCTGCPPLHVAGMPCISASFHT 296  
 Db 3 GLECDGKVNICKCKKOFPSFDIGNDWIIAPSGYHANCCEGCPSHIAGTSGSSLSFHS 62

Db 63 TVINHYRMGHSPFANLKSVCVPTKLRPMMSMLYDDGQNIKKDIQNMIVBECGC 117

## RESULT 15

OY 234 RRGIDCGGS-RMCCROEFFVDFREIGNDWIIIOPEGYAMNFCCTGCPPLHVAGMPCISASFHT 292  
 Db 15 RGSFECGCGNGGGLCCROOFYIDFRLIGNDWIIAPAGYGVNCEGSCPAYMAGVGSAS 74

Query Match  
 Best Local Similarity 19.3%; Score 357; DB 13; Length 138;  
 Matches 61; Conservative 24; Mismatches 31; Indels 4; Gaps 3;

OY 234 RRGIDCGGS-RMCCROEFFVDFREIGNDWIIIOPEGYAMNFCCTGCPPLHVAGMPCISASFHT 292  
 Db 15 RGSFECGCGNGGGLCCROOFYIDFRLIGNDWIIAPAGYGVNCEGSCPAYMAGVGSAS 74

Search completed: October 12, 2002, 02:08:42  
 Job time: 44 secs

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